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FILING DATE
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Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 66687, A
Sequence 43, Appl
                                                                                                                                                    September 8, 2005, 02:10:48; Search time 89.0685 Seconds (without alignments) 2104.671 Million cell updates/sec
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Sequence 26, App
Sequence 24, Appl
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                                                                                                                                                                                                                                                                                                               1 MDATTGDFTALQXAVKQMAT.....GANIAGFTKVADAVKAQGAV 476
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1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_MBW PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

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9: \cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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12: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-282-122A-66687
US-10-988-943-43
US-10-282-122A-65129
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US-09-070-844-24
6 US-10-627-886-24
US-09-070-844-4
US-09-070-844-4
US-09-070-844-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1774312 seqs, 393823214 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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											1185	1184	1182.5	1300 5	9-	1178

ALIGNMENTS

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RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPWGGGKGGSDFDPKGKSDAEVWRFCQSFWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVL FVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSOGYVYEPNG
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Patent No. US20020062495A1

GENERAL INCPORMATION:

APPLICANT: Schnidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n 100.0%; Score 2465; DB 16; Similarity 100.0%; Pred. No. 5.1e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-CCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-CCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-627-886-26
                                                                                                                                                                                                                                          NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (352) 372-5800
INFORMATION FOR SEQ 1D NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 476, Conservative
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US-09-070-844-24
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DS OF USE
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                                                                                                                                                                                                                                                                                                                     Gaps
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Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                      Length 476;
                                                                                                                                                                                                                                                                                                                   Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELATING TO THE .- AND -SU
DEHYDROGENASES AND METHODS
                                                                                                                                                                                                                                                                 100.0%; Score 2465; DB 9;
100.0%; Pred. No. 5.1e-221;
iive 0; Mismatches 0;
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ADDRESSE: Saliwanchik & Saliwanchik STRET: 2421 N.W. 41st Street, Sulte A-1 CITY: Galnesville STATE: Florida COUNTRY: USA
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APPLICATION NUMBER: US/10/627,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-627-886-26
; Sequence 26, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                   TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-8800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 476; Conservative
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                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                    US-09-070-844-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVSLOPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
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                                                                                                                                                                                                                                                                                            SOFTHARE: PEC-DOS/MS-DOS
SOFTHARE: PACEDOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
APPLICATION NUMBER: 08/725,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2465; DB 9;
100.0%; Pred. No. 5.3e-221;
iive 0; Mismatches 0;
AUDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-NAC CURPARE: Patenty-CIPPERS P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-8800
INFORMATION FOR SEC ID NO: 24:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 476; Conservative
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RESULT 4 US-10-627-886-24

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                                                                                      Miller, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
THE - AND -SUBUNIES OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 MDATIGDFIALQKAVKQMATKAGIEGLVHGIKNPDVRQLLIEIFMKDPEQQEFMQAVREV
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100.0%; Score 2465; DB 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-221;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                         NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REGISTRATION NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-0CT-95
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-627-886-24
Sequence 24, Application US/10627886
Publication No. US20840128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 487 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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FTREQLQAVQDMKKKNISARISEYKSDTAVYVGDRKKPWELDCQVDIAFPCATQNEIDEH 396
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APPLICANT: Schmidt, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: TO THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                             GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                          397 DAELLIKHGCOXYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                     LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                      FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                        421 LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                                                                                                     LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 512
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS POPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATE:
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-95
APPLICATION NUMBER: 08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2465; DB 16; 100.0%; Pred. No. 5.7e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UF-155CD3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-627-886-4
; Sequence 4, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Best Local Similarity
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                                                                                                   372 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 156
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                                                                                                                                                            421 LIWITREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFIKVADAVKAQGAV 476
                                                                                                                                                                                           1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: S421 N W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 2465; DB 9;
Best Local Similarity 100.0%; Pred. No. 5.7e-221;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/ASENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFRENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09070844 Patent No. US20020062495Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schmidt, Robert R. APPLICANT: Miller, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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amino acid
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MOLECULE TYPE: protein
US-09-070-844-4
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APPLICATION NUMBER: 09/070,844
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Publication No. US20040128710A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                  : 526 amino acids
amino acid
                                                                                                                            Best Local Similarity 100.
Matches 476; Conservative
    SEQUENCE CHARACTERISTICS
                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                              US-09-070-844-2
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US-10-627-886-2
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                                                                                                             LORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY 240
                                                                                                                                                                                                                                                                                                     AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
                                                                                                                                                        GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDPDPKGKSDAEVMRFCQSFMTE 180
                                                                                                                                                                                                                                                                                   GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
                                                                                                                                                                                                                                                                                                                                                                  337 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH 396
                                               Sequence 2, Application US/09070844

Patent No. US20020062495A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: DEHYPROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STREET: Plorida

COUNTRY: USA
                                                                                                                                                                            157 GLRFHDSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSPMTE
                                                                                                                                                                                                                                       217 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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                               MDATTGDFTALQKAVKQMATKAGTEGLVHGI KNPDVRQLLTEI FMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 476
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   Indels
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ZIP: 32606

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
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 0; Mismatches
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CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
RECISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
 Conservative
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TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                      171 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
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                                                                                                                     1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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      Length 526;
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ADDRESSEE Saliwanchik & Saliwanchik STREET: 2421 N W 4 1st Street, Suite A-1 STREET: 2421 N W 4 1st Street, Suite A-1 CITY: Cainesville STATE: Florida CUNTXY: USA ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: PIN PC Compatible COMPUTER: PARTIC SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                            Indels
100.0%; Score 2465; DB 9;
100.0%; Pred. No. 5.9e-221;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <UNKNOWN>
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SEQ ID NO 66687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQSYGGSEIRPEATGY
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FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-0CT-95
ATTORNEY/AGENT INFORMATION:
NAME: LIOYG, Jeff
RECISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: 19.55CD3
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPAX: (352) 375-8100
TELEPAX: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66687, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Wang, Liangsu
APPLICANT: Manone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblesn, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
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APPLICANT: Ku, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLICATION NUMBER: 60/206,848
PRIOR PLICATION NUMBER: 60/203
PRIOR PLICATION NUMBER: 60/203
PRIOR PLICATION NUMBER: 60/203
PRIOR PLICATION NUMBER: 60/203
PRIOR PLICATION NUMBER: 60/230,347
PRIOR PLICATION NUMBER: 60/230,347
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PRIOR PLICATION NUMBER: 60/230,347
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-112-22
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-22-26
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NUMBER OF SEQ ID NOS: 78614
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US-10-282-122A-66687
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2008-03-22
PRIOR PLICATION NUMBER: 60/191,078
PRIOR PLICATION NUMBER: 60/201,727
PRIOR APPLICATION NUMBER: 60/201,727
PRIOR APPLICATION NUMBER: 60/201,727
PRIOR APPLICATION NUMBER: 60/201,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 444;
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US-10-282-122A-66041
; Sequence 66041, Application US/10282122A
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US-10-282-122A-65129
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                                       Sequence 43, Application US/1098943
Publication No. US20050176085A1
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
TITLE OF INVENTION: COMPLEX MIXTURES.
FILE REFERENCE: Proteomics CU2003-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT PILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
ERNGTH: 444
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Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Manone, Carlos
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Prawick, John
APPLICANT: Prawick, John
APPLICANT: Porsyth, R.
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US-10-282-122A-65129
       US-10-988-943-43
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302 YFENQKPWGV--AAEIALPCATQNELDEEAAKTLLANGCYVVAEGANMPSTLGAVEQFIK 359
                                                                    AGIIYCPGKAANAGGVAVSGLEMTQNRMSLAWTREEVRDKLERIMKDIYDSAMGPSRRY- 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 444;
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Christoph
TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
FILE REPERENCE: GJE-6436
CURRENT APPLICATION NUMBER: US/10/275,026A
CURRENT PILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/GB01/02003
PRIOR PLING DATE: 2001-05-08
PRIOR PLING DATE: 2000-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.5%; Score 1294.5; DB 15; Lengt Best Local Similarity 57.1%; Pred. No. 1e-111; Matches 256; Conservative 72; Mismatches 105; Indels
                                                                                                                                                        |: ||||||| |||||||| KVGDTVNYVNGANIAGFVKVADAMLAQG 443
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                                                                                                                              ----NVDLAAGANIAGFTKVADAVKAQG
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US-10-282-122A-67538
; Sequence 67538, Application US/10282122A
                                                                                                                                                                                                                                                                           Sequence 152, Application US/10275026A Publication No. US20040087770A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2 SEQ ID NO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 214
                                                                                                                                                                                                                                      RESULT 13
US-10-275-026A-152
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5%; Score 1294.5; DB 15; Length
57.1%; Pred. No. 1e-111;
tive 72; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Neisseria meningitidis US-10-282-122A-66041
                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
US20040029129A1
                                                                                                                                                               Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1'
Matches 256; Conservative
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APPLICANT:
APPLICANT:
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272 242

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369, 493
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR PILING DATE: 2002-02-21
                                                                                             94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 153
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                                                                 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM--GPSRRYN 451
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Matches 258; Conservative
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APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/19/078
PRIOR FILING DATE: 2000-03-02-03
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PRILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
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                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
US20040029129A1
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Best Local Similarity 58.2%;
Matches 259; Conservative 5
                                                                                                                                                                                                                                                         Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Sequence 24, Appl
Sequence 4, Appli
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Sequence 20646, A
Sequence 20646, A
Sequence 3184, Ap
Sequence 3184, Ap
Sequence 11, Appli
Sequence 11, Appli
Sequence 7937, Ap
Sequence 657, Ap
Sequence 657, Appli
Sequence 657, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 17183, Ap
Sequence 17183, Ap
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-8141-24

US-08-828-451-24

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US-08-828-451-2

US-08-913A-2

US-09-328-352-5725

US-09-328-352-5725

US-09-384-110-4489

US-09-886-640-3

US-08-886-640-3

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US-09-881-10-4489

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US-09-10-33-11

US-09-10-33-11

US-09-543-681A-6657

US-09-543-681A-6657

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Maximum Match 100%
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Sequence 832, App
Sequence 7622, Ap
Sequence 7623, Ap
Sequence 17482, A
Sequence 21, Appli
Sequence 2, Appli
Sequence 2, Appli
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23, Appl
832, App
7622, Ap
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20, Appl
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US-09-239-303-9
US-09-2540-12638
US-09-22540-12638
US-09-328-352-6130
US-09-489-0198-1395
US-08-461-9908-22
US-08-461-9908-22
US-08-518-092-1153
US-09-538-092-1153
US-09-549-016-7622
US-09-949-016-7622
US-09-949-016-7623
US-09-948-796A-17482
US-09-918-752A-991
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
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REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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MOLECULE TYPE: protein
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                                                             Gaps
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APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OP USE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2411 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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      Length 476;
                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
Query Match 100.0%; Score 2465; DB 2; Best Local Similarity 100.0%; Pred. No. 7.2e-225; Matches 476; Conservative 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMINICATION INFORMATION:
TELEFHONE: (904) 372-8100
TELEFAX: (904) 372-8100
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 24, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
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linear
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STATE: Florida
COUNTRY: USA
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US-08-541-033A-4
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| Patent No. 5985634
| GENERAL INFORMATION:
| APPLICANT: Schmidt, Robert R. APPLICANT: Schmidt, Robert R. APPLICANT: Miller, Philip
| TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
| TITLE OF INVENTION: BELATING TO THE - AND -SUBGNITS OF GLUTAMATE
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| CORRESPONDENCE ADDRESS: ALIWANCHIK & Saliwanchik & Sa
                                                                                                                                                                                                                                                                                                                  12 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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                                                                                                                                                                                    Length 487;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn NaTA:
APPLICATION NUMBER: US/08/828,451
FLING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                               Query Match 100.0%; Score 2465; DB 2; Best Local Similarity 100.0%; Pred. No. 7.5e-225; Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               7.5e-225;
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                               US-08-541-033A-24
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US-08-828-451-24
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Patent No. 587941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DELYDROGENASES AND METHODS OF USE
TITLE OF INVENTION: DELYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallwanchik & Saliwanchik
STATE: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
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100.0%; Pred. No. 7.5e-225;
ative 0; Mismatches 0;
                                       36,965
FR: UF155
                   NAME: Whitlock, Ted W.
REGISTRATION UNDRER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 476; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 MDATTGDFTALOKAVKOMATKAGTEGLVHGIKNPDVRQLLIEIFMKDPEQGEFMQAVREV 96
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Patent No. 5985634
GENERAL INVENTATION
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DELYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                          Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                        0, Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                       ; Score 2465; DB 2;
; Pred. No. 8.1e-225;
0; Mismatches 0;
                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMINICATION INFORMATION:
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 476; Conservative 0;
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                      US-08-541-033A-4
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100.0%; Pred. No. 8.1e-225;
iive 0; Mismatches 0;
                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08541033A
; Patent No. 5879941
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlook, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFLE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 375-8100
TELEFAX: (904) 375-8100
TELEFAX: (904) 375-5100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 512 amino acids
amino acid
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Matches 476; Conservative
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
Florida
                       USA
                                            32606
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US-08-541-033A-2
                  COUNTRY:
ZIP: 326
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240 276 360 396

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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
                                                     ; Sequence 2, Application US/08828451; Patent No. 5985634; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATONEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION UNDBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 375-800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 anino acids
TYPE: amino acids
TOPPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                     32606
                       RESULT 8
US-08-828-451-2
                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DABLLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOUE POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DERYDROGENASES AND METHODS OF USE
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526;
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                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2465; DB 2;
100.0%; Pred. No. 8.4e-225;
ive 0; Mismatches 0;
                                                                                                                   ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                APPLICALLON ATERIA PLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-5800
TELEPAX: (504) 372-5800
TELEPAX: (504) 372-5800
TELEPAX: (904) 372-5800
TELEPAX: (904) 372-5800
TELEPAX: (904) 372-5800
TELEPAX: (904) 372-5800
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Best Local Similarity 100.
Matches 476; Conservative
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240 51 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 110 300 360 61 AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120 121 .GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGKGGSDFDPKGKSDAEVMRFCQSFMTE 180 290 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH 410 09 LORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY LORHISYVODVPAGDIGVGAREIGYLFGGYKRITKNYTGVLTPKGQEYGGSEIRPEATGY GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYBPNG 1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH Gaps APPLICANT: Schoolt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: Saliwanchik & Saliwanchik
CITY: Gainesville
STATE: Florida ö Query Match 100.0%; Score 2465; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 8.4e-225; Matches 476; Conservative 0; Mismatches 0; Indels 0 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451 351 g

78 20 130 198

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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3884, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID SECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBACE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLK 258
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US-09-328-352-5725
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GENERAL INFORMATION:
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US-09-134-000C-3884
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20646
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                                       334 DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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) Sequence 5725, Application US/09328352

) Patent No. 6562958
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US-09-252-991A-20646
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US-09-252-991A-20646
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Best Local Simil
Matches 263; C
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                                                                                   188 NQFDAGVLTGKPLGFGGSLIRPEATGYGLVYYTEEMLKANGNSFAGKKVVISGSGNVAQY
                                                           214 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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Best Local Similarity 54.0%; Pred. No. 4.3e-105;
Matches 241; Conservative 67; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lightfoot, David
APPLICANT: Long, Lynn
APPLICANT: Lightfoot, Maria V
TITLE OF INVENTION: PLANTS CONTAINING THE 
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kokulis, Paul K.
REGISTRATION WINBER: 16,773
REFERENCE/DOCKET NUMBER: 81163/241766
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: OLDER SCALES

ZIP: 10005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,640
FILING DATE: 01-UUL-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                       424 KDYLAGANIAAFENVANAMIAQGIV 448
                                                                                                                                                                                                                                                                                                                                                               453 -DLAAGANIAGFTKVADAVKAQGAV 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,058
FILING DATE: 02-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08886640 Patent No. 5998700
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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US-08-886-640-3
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Sequence 4469, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
TITLE OF INVENTION: Demonsiae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Polarios 100-05-26

CURRENT APPLICATION NUMBER: US/09/583,110

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4489

TENTH: 448
                                                                                                                                                    247 AMEKATELGATVITCSDSSGFVYDPEGI---DVALVKELKEKNRE-RISKYVETRKGATY 302
                                                                                                                                                                                                                                                                                                                                                                                                                                     332 VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 391
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                                                                                                                              94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 153
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                                                                             36 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                   63; Mismatches 123;
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 No. 2.9e-108;
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 55.9%; Pred.
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                   Matches 250; Conservative
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Best Local Similarity
Matches 248; Conserv
Best Local Similarity
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67 WVDDRNQIQVNRAMRVQPSSAIGPYKGGMRFHPSVNLSILKFLGFEQTFKNALTTLPMGG 126
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                                   WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFRQIFKNSLTTLPMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 175. S. JEPFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ONO, BIJI
APPLICANT: TSUJIMOTO, NOBUHARU
APPLICANT: MATSUI, KAZUHIKO
APPLICANT: KURAHSHI, KAZUHIKO
ATILLA OF INVENTION: MUTANT AND METHOD FOR PRODUCING
TITLE OF INVENTION: L-GLUTAMIC ACID BY PERMENTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,193A FILING DATE: 09-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 NVDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/08370193A; Patent No. 5573945
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-3220
TELEPAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
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MEDIUM TYPE: Floppy
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                                1 ESFLAHVQKRDPNQTEFAQAVREVMTTLWPFLEQNPKYRQMSLLERLVEPERVIQFRVV 66
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VRQLLTEIPMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIPKQIVEPERVITFRVS
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APPLICANT: Lightfoot, David A.
APPLICANT: Lightfoot, Main B. Vidal
APPLICANT: Lightfoot, Main B. Vidal
TITLE OF INVENTION: PLANTS CONTAINING THE GGNE AND
TITLE OF INVENTION: METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: 0.0.1. Led States of America
ZIP: 20005-3918
CONDUTER: LBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPAT
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Best Local Similarity 54.0%; Pred. No. 4.3e-105;
Matches 241; Conservative 67; Mismatches 128;
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SOFTWARE: MS WOLD
SOFTWARE: MS WOLD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,235
FILING DATE: 27-UN-1997
CLASSIFICATION: 800
INPORMATION POR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 residues
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: not relevant
"DOLOGY: not relevant
"DOLOGY: not relevant
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Patent No. 6329573
GENERAL INPORMATION:
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                                                                                                                          36 VROLLTEIFMKDPEQOEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 93
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                                                                                                                                          Query Match

48.7%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 5.4e-105;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-370-193A-11
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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8; Search time 86.1641 Seconds (without alignments)
2828.902 Million cell updates/sec 8, 2005, 02:12:18 OM protein - protein search, using sw model September Run on:

US-10-627-886-26 2465 1 MDATIGDFTALQKAVKQMAT......GANIAGFTKVADAVKAQGAV 476

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Describution	P28998 chlorella s	Q8ilf7 plasmodium	Q7rq39 plasmodium		Q7r3n7 giardia lam		Q9hvj7 pseudomonas		Q9jt56 neisseria m	Q88q23 pseudomonas		Q7yzu7 trichomonas	_	Q8ilt0 plasmodium	Q9txs8 plasmodium		-		Q8g610 bifidobacte	Q8ge72 ruminococcu	Q6Fd67 acinetobact	Q8xk85 clostridium	Q8e4j6 streptococc	_	P43793 haemophilus	Q8dyy7 streptococc	O61083 trypanosoma	-	_	Q9cpj4 pasteurella	~
	£		DHE4 CHLSO	Q8ILF7	Q7RQ39	Q7YZU9	Q7R3N7	DHE4 GIALA	Q9HV <u>J</u> 7	Q9JY71	Q9JTS6	088023	Q9Z3C4	Q7YZU7	096940	Q81LT0	Q9TXS8	Q9GTK5	Q6S143	Q7RGT5	Q8G6L0	Q8GE72	Q6FD67	Q8XK85	Q8E4J6	Q835G2	DHE4_HABIN	Q8DY <u>Y</u> 7	061083	Q65W57	Q8DUL2	Q9CPJ4	DHE3_BACTN
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مد	Query	יומיכוו	99.1	55.8	55.2	53.9	53.9	53.7	53.1	52.8	52.5	52.2	52.1	52.1	51.9	51.9	51.3	51.3	51.0	50.9	50.7	50.7	50.7	50.4	50.3	50.3	50.2	50.2	50.1	20.0	49.9	٠	49.7
	Score	2 1	2444	1375	1361	1328	1327.5	1324.5	1309	1300.5	1294.5	1287.5	1285	1284.5	1279.5	1279.5	1265	1264	1257	1253.5	1250.5	1250.5	1249.5	1241.5	1240.5	1239.5	1238	1236.5	1234	1231.5	1230.5	m	1225.5
•	Result		1	2	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	26	27	28	29	30	31

Q9aiw1 streptococc P95544 prevotella Q84pg0 streptococc Q97qb4 streptococc Q9kb34 bacillus ha Q7vsn6 bordetella Q7veu7 bordetella Q84g1 bordetella Q88xm9 lactocodes Q88xm9 lactocodes Q80370 escherichia Q60996 trypanosoma Q60996 trypanosoma Q60996 trypanosoma Q60996 coletale
09AIW1 DHE4 PRERU 08DEG0 0970B4 0970B4 07VSN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 097SN6 099F6
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlorella sorokiniana.
Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorellaceae, Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-92032762; PubMed=1718478;
Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;
Tock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;
Thuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella
                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 By similarity.
57529 MW; A35FE730E5FEF974 CRC64;
                                                          523 AA
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                                                          STANDARD;
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P28998;
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SEQUENCE
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DHE4_CHLSO
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 GGSDFDPKGKSENRILKFCQSFMTNLFRYIGPNTDVPAGDIGVGGREIGYLFGQYKKLKN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 BLLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 ENQKPWNIPC--DIAFPCATQNEINENDADLFIQNKCKMIVEGANMPTHIKALHKLKQNN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 IIYCPGKAANAGGVAVSGLEMTQNRMSIAWTREEVRDKLERIMKDIYDSAMGPSRRY--N 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 EKLIEKGAIVLTMSDSNGYILEPNGFTKEQLNYIMDI-KNNQRLRLKEYLKYSKTAKYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 GGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                                                                                                                                                                                                                                                                                                   36 VRQLLTBIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
                                               PS00074; GLFV DEHYDROGENASE; 1.
510 AA; 57343 MW; AC400045297AC64F CRC64;
                                                                                                                                                                              55.8%; Score 1375; DB 2; 60.0%; Pred. No. 2.7e-88; iive 66; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 VDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 486 SDLVAGANIAGFLKVADSFLEQGGL 510
                 PRINTS; PR00082; GLFDHDRGNASE.
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                                                                                                                                                                                                                             dest Local Simi
Matches 267;
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                                                                                                                                                                                                                     48 MDATTGDFTALQKAVKQMATKAGTBGLVHGIKNPELRQLLTEIFMKDPEQQEPMQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 LQRHISYVQDVPAGDIGVGARBIGYLPGQYKRITKNYTGVLTGKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                              1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQOEFMQAVREV
                                                                                                                                                                                                                                                                                                                                          61 AVSLOPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glutamate dehydrogenase, putative.
0RPMames=Pl4 0286;
Plasmodium falciparum (1solate 3D7).
Eukaryota, Alveolata; Aplcomplexa; Haemosporida; Plasmodium.
NCBL_TAXID=36329;
                 Length 523;
                                                                                           Indels
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7
             Score 2444; DB 1;
Pred. No. 1.7e-163;
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Nature 419:498-511(2002).
EMB1. AE014620; AAN36899.1; -
HSSP; P24295; 1AUP.
        99.14;
Query Match
Best Local Similarity 99.2
Matches 472; Conservative
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"Genome sequence and comparative analysis of the model rodent malaria Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Sin B.B., Kooij T.W., Pertea M., Sin B.B., Kooij T.W., Pertea M., Sin W. J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Shetreon J.D., Pop M., Koack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Vanningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J.; parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data. Plasmodium yoelii yoelii. Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium. NCBI_TaxID=73239; 01-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                             Length 446;
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Last annotation update)
                               GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLEV dehydrog.
InterPro; IPR006096; GLEV dehydrog.C.
InterPro; IPR006097; GLEV dehydrog_N.
Pfam; PF00208; GLEV dehydrog_N.
Pfam; PF02812; GLEV dehydrog_N; 1.
PROSITE; PS00074; GLEV DEHYDROGENASE; 1.
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EMBL, AACB01000014; EAA41919.1; -.
HSSP; P24295; LAUP.
GO; GO:0016491; F:oxidoreductase activity; IEA
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(TrEMBLrel. 26, I
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Best Local Similarity 58.6%
Matches 262; Conservative
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           HSSP; P24295; 1AUP
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STRAID=ATCS 50380;
PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
"Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes.";
EMC Evol. Biol. 3:14-14(203).
EMBL; AF533884; AAP83851.1; -.
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Eukaryota, Diplomonadida, Hexamitidae, Hexamitinae, Spironucieus.
NCBI_TaxID=103874;
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Last annotation update)
                                                 GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; F:amino acid metabolism; IEA.
InterPro: IPR005135; Exo endo phos:
InterPro: IPR006095; GLFV dehydrog.
InterPro: IPR006095; GLFV dehydrog.
InterPro: IPR006095; GLFV dehydrog.
Pfam; PF03172; Exo endo phos; 1.
Pfam; PF021812; GLFV dehydrog. 1.
Pfam; PF021812; GLFV dehydrog. 1.
Pfam; PF021812; GLFV dehydrog. 1.
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
Glutamate dehydrogenase (Fragment).
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EMBL; AABL01000331; EAA20557.1;
HSSP; P24295; 1AUP.
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Matches
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                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parasitology 112:1-12(1996).
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
+ NH(3) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK
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                                                                         SUBUNIT: Homohexamer (By similarity). SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
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67; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 125 By similarity.
249 249 I -> L (in Ref. 2).
449 AA, 49766 MW; 5497B35209B549F6 CRC64;
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(TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.7%; Score 1324.5; 58.2%; Pred. No. 8.1e
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HSSP; P24295; LAUP.
InterPro; PR006099; GLFV dehydrog.
InterPro; IPR006099; GLFV dehydrog.C.
InterPro; IPR006099; GLFV dehydrog.C.
InterPro; IPR006097; GLFV dehydrog.N.
Pfam; PF002028; GLFV dehydrog.N.
PRINTS; PR00082; GLFDHHRGNASE;
PROSITE; P800074; GLFV DEHYDROGENASE; 1.
NADP; Oxidoreductase.
ACT SITE 125 125 By similarity.
CONFLICT 249 249 I -> L GIN Reference.
SEQUENCE 449 AA, 49766 MW; 549783520985
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Matches 260; Conservative
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 EFTGVLTGKNVKWGGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKNVLLSGSGNVAQFAC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKS---DTAVYV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 EKLIQLGAKVLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDRRKPWE-LDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G--KKPWECFEGQVDCIMPCATQNEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 KGVMYGPAKASNAGGVSVSGLEMSQNSVRLQWTAEEVDQKLRGIMRGIFVACRDTAKKYG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 451
                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                          216 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                                                                                                                                                                                                                                                                                            36 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPEKVITFRVSWL
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MEDLINE=92218410; PubMed=1559991;
Yee J., Dennis P.P.;
Tieolation and characterization of a NADP-dependent glutamate dehydrogenase gene from the primitive eucaryote Giardia lambia.";
J. Biol. Chem. 267:7539-7544(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular genetic analysis of Giardia intestinalis isolates at glutamate dehydrogenase locus.";
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MEDLINE=96155200; PubMed=8587793;
Monia P.T., Mayrhofer G., Andrews R.H., Homan W.L., Limper L.,
                                                                                                                                                                                                                                                 2; Length 449;
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P28724; Q24961;
P28724; Q24961;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
29-MAR-2004 (Rel. 43, Last annotation update)
dependent glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)
dependent glutamate dehydrogenase).
Glardia lamblia (Glardia intestinalis).
Eukaryota, Diplomonadida; Hexamitidae; Glardiinae; Glardia.
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                    PROSITE, PS00074; GLFV DEHYDROGENASE; 1.
SEQUENCE 449 AA, 49734 MM, 2397B34FBEBCAEE2 CRC64;
                                                                                                                                                                                                                                                                                              66; Mismatches 111;
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                                                                                                                                                                                                                                              53.9%; Score 1327.5; Di
58.4%; Pred. No. 5e-85;
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  GO:0006520; P:amino acid metabolism;
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                    InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV dehydrog_N.
Pfam; PF002812; GLFV dehydrog, 1.
Pfam; PR02812; GLFV dehydrog_N.
PRINTS; PR00082; GLFPHDRGNASE.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.4°
Matches 261, Conservative
                                                                                                                                                                                              SEQUENCE
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
Mickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 AA; 48856 MW; 643EB12BC84F3418 CRC64;
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004872; AAG07976.1; -.
PIR; H83072; H83072.
HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006099; GLFV dehydrog_C.
Pfam; PF00208; GLFV dehydrog_N.
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                           Glutamate dehydrogenase.
Name=gdhA; OrderedLocusNames=PA4588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 59.29
Matches 263; Conservative
                                                                                 Pseudomonas aeruginosa.
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGDRRKFWWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 YFEKQKPWGV--AABIALPCATQNELDEBAAKTLLANGCYVVAEGANMPSTLGAVEQFIK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                            MEDINES 2017575; PubMed=10710307; DOI=10.1126/Science.287.5459.1809; MEDINES.2017575; PubMed=10710307; DOI=10.1126/Science.287.5459.1809; Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H.M., Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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                                                                                                                                                      OrderedLocusNames=NMB1710;
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P24295; IAUP.
TIGR; NMB1710; -.
GO; GO: NO16491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.8%; Score 1300.5; DB 57.4%; Pred. No. 3.9e-83.ive 72; Mismatches 10.
   444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.C.
InterPro; IPR006097; GLFV dehydrog.N.
Pfam; PF020008; GLFV dehydrog.N.
PFINYS; PR00082; GLFV dehydrog N; 1.
PRINYS; PR00082; GLFDHDRGNASE.
PROSTIF; PS00074; GLFV DEHYDROGENASE; 1.
Complete proteome.
SEQUENCE 444 AA; 48490 MW; 8B2CFCCA895EF
                                                                           01-0CT-2000 (TrEMBLrel. 15, Last sequen 01-JUN-2003 (TrEMBLrel. 24, Last annota Glutamate dehydrogenase, NADP-specific.
                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:1809-1815(2000).
EMBL; AE002521; AAF42057.1; -.
PIR; H81050; H81050.
                                                      (TEMBLrel, 15, (Trembrel, 15, (Trembrel, 15,
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PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=491;
                                                      01-OCT-2000
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332 VGDRRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: 00:0016491; F:oxidoreductase activity; IEA.
GO: 00:0016510; F:oxidoreductase activity; IEA.
GO: 00:0016520; F:omino acid metabolism; IEA.
InterPro: IPR006095; GLFV_debydrog.
InterPro: IPR006096; GLFV_debydrog.
Pfam; PF00209; GLFV_debydrog.
Pfam; PF00209; GLFV_debydrog.
PRINTS; PR00082; GLFV_debydrog.
PRINTS; PR00082; GLFV_debydrog.
PROSITE; PS00074; GLFV_DEBYDROGENASE; 1.
Complete proteome.
SEQUENCE 449 AA; 48871 MW; EF173386ABC89627 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $
                                                                                                                                                                                                                                                                                                                                   416 KVGDTVNYVNGANIAGFVKVADAMLAQG 443
                                                                                                                                                                                                                                                                                                  ----NVDLAAGANIAGFTKVADAVKAQG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutamate dehydrogenase.
Name=gdhA; OrderedLocusNames=PP0675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas.
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58.2%;
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Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=160488;
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01-JUN-2003 (
01-OCT-2003 (
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153 GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 YCAELLLEKGAIVLSLSDSQGYYYEP-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 SWLDDAGNLQVNRGPRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=22491 / Serogroup A / Serotype 4A;

MEDLINE=2022556; PubWed=10761919; DOI=10.1038/35006655;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,

Klee S.R., Morellid G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,

Rajandream M.A., Rutherford K.M., Slmmonds M., Skelton J.,

Whitehead S., Sprat B.G., Barrell B.G.,

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO, GO:0004554; F:glutamate dehydrogenase (NADP+) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016591; F:oxidoreductase activity; IEA.
GO; GO:0006501; F:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
Pfam; PF02812; GLFV dehydrog_N; 1.
PRINTS; PR00082; GLFV dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE; 1.
Complete proteome; Oxidoreductase.
SEQUENCE 444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;
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52.5%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 1e-82;
Matches 256; Conservative 72; Mismatches 105; Indels 15;
                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Glutamate dehydrogenese (EC 1.4.1.4).
Name=gdlh; OrderedLocusNames=NNA1964;
Naisseria meningitidis (serogroup A).
Bacteria; Porteobacteria; Betaproteobacteria; Neisseriales;
NAISSETIACEASE; Neisseria.
                                                                                                                                                                                                                                                                                                                                   444 AA.
                                                                                                     474
                                                                                                                                         16 KVGDTVNYVNGANIAGFVKVADAMLAQG 443
                                                                                                 451 ----NVDLAAGANIAGFTKVADAVKAQG
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis 22491.";
Nature 404:502-506(2000).
EMBL; AL162797; CAB85184.1; -.
PIK; B81825; B81825.
HSSP; P24295; 1AUP.
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Q9JT56;
                                                                                                                                                                                                                                                       RESULT 9
Q9JT56
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                                                                                                                                                                                                                                                                                                                           360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG 415
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                                                                             68 WYDDQGKVQYNRGYRIQMSSAIGPYKGGLRFHPSYNLSYLKFLAFEQVFKNSLTSLPMGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 213
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Nelson K.E., Wahnel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Wahnel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Praser C.M., Tuewer J.A., Timmis R.N., Duesterhoeft A., Tuemmler B.,
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 449;
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124

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245 AARKVMEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELK----NARAGHPRDGVEQFSL 300
                                                                                                                                                                                                                                                                                                                                                                                                                               301 QFLEGVPPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFL 358
                                                                                                                                                                                                                                                                                                  274 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDT---AV 330
                                                                                                                                                                                                                                                                                                                                                                                                 331 YVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 KAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRR 449
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                              125 GKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL
                                                                                                                                                                                                                                94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
                                                                                                   GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
                                                                                                                                                                                                    214 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDUBLICE FROM N.A.

SEQUENCE FROM N.A.

Anderson J.O., Roger A.J.;

Anderson J.O., Roger A.J.;

Anderson J.O., Roger A.J.;

Anderson J.O., Roger A.J.;

Transfer within and between prokaryotes and eukaryotes.";

Transfer within and between prokaryotes and eukaryotes.";

EMBL; AF533886; AAB93853.1; -.

InterPro; IPR006095; GLFV dehydrog.

INTERPO; IPR006095; GLFV dehydrog.

INTERPO; IPR006095; GLFV dehydrog.

R PROSITE; PS00074; GLFV DEHYDROGENASE; 1.

INDN TER.

INDN TER.

SEQÜENCE 437 AA; 47861 MW; 75205554DAFBEF96 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Parabasalidea; Trichomonada; Trichomonadida;
Trichomonadidae; Trichomonadinae; Trichomonas.
NCBI_TaxID=5722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 YNVDLAAGANIAGFTKVADAVKAQGAV 476
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Best Local Similarity 59.0*
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=gdh;
Trichomonas vaginalis.
                                                                                                      154
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                                                                                                                       248 AARKVMDLGGKVISLSDSEGTLYAEAGLTDAQWDALMELKNVKR-GRISELAGQFGLEFR 306
                                                                                              CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 333
                                                                                                                                                                                                                             394 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM--GPSRRYN 451
                                                                                                                                                                                                                                                                                                                         36 VRQLLITEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                         188 ANQFISVLIGKGMIYGGSLIRPEAIGYGCVYFAEEMLKRQDKRIDGRRVAVSGSGNVAQY
                                                                                                                                                                                            DRRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016591; F:oxidoreductase activity; IEA.
GO; GO:0006591; Branino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006095; GLFV dehydrog_C.
FinerPro; IPR006095; GLFV dehydrog_N.
Fam; PF00208; GLFV dehydrog_N.
Fram; PF002081; GLFV dehydrog_N.
Fram; PF002081; GLFV dehydrog_N.
Fran; FP00082; GLFDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                           <u>=</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
NADP-glutamate dehydrogenase (EC 1.4.1.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     452 VDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ansari F.;
Thesis (1994), University of London,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PAC1, and PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=PAC1;
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                                                                                              274
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Best Local &
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                                                                                                                                                                      185 ISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVL 244
                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                          305 QLQAVQDMKKKONNSARISEY -- KSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDA 362
                                                                                                                                                                                                                                                                                                                                                                                     353
                                                                                                                                                                                                                                                                                                                                                                                                                             ELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413
                                                                                                                                                                                                                                                        FVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTRE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.W., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angluol S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Pairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Praser C.M., Barrell B.;
                      178 IGPCTDVPAGDIGVGGREIGYLYGQYKKIVNSFNGTLTGKNVKWGGSNLRVEATGYGLYY
                                                                                                                                                                                                                                                                                 FVLEVIKSLNI PVEKQTAVVSGSGNVALYCVQKLLHLNVKVLTLSDSNGYVYEPNGFTHE
  QPVFEKRPELLP1FKQ1VEPERV1TFRVSWLDDAGNLQVNRGFRVQYSSA1GPYKGGLRF
                                                                                                                                                                                                                                                                                                                                                                     354 KILQKNGCILVGEGANMPSTVDAINLFKSNNIIYCPSKAANAGGVAISGLEMSQNFQFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTRETVDEKLKEIMRNIFIACSENALKYTKNKYDLQAGANIAGFLKVAESYIEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the human malaria parasite Plasmodium falciparum.";
Mature 419:498-511(2002).
EMBL; AR014818; AAN36776.1; -.
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%; Score 1279.5; DB 2; Length 55.6%; Pred. No. 1.3e-81; ive 62; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52546 MW; 50A37C23484C387A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADP-specific glutamate dehydrogenase.
ORFNAmes-PP14 0164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
Pfam; PF00208; GLFV dehydrog; 1.
PRINTS; PR00012; GLFV DEHYDROGENASE; 1.
PROSTITE; PR00014; GLFV DEHYDROGENASE; 1.
SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A GR
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Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                          402
                                                                                                          286 LSLSDSQGYVYEPNGFTREQLQAVQDMKK--KNNSARISEYKSDTAVY-VGDRRKFWELD 342
                                                                                                                                                                                                              244 VŚCŚDŚHĠALIFKDGMTKEHLDĀVMHIKNVARTELKKIŚELFPDLKGYEYIDGKSIWACE 303
                                                                                                                                                                                                                                                                                 NAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAG 462
                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum. Cloning, expression and characterization of the malarial enzyme."; Eur. J. Biochem. 258:813-819(1998).
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                   5 TGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSL
SDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKG
                                                                                  226 QEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIV
                                                                                                                                                                                                                                                          343 CQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog.
Pfam; PF020812; GLFV_dehydrog.
PFam; PF020812; GLFV_dehydrog.
PROSITE; PS00004; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
Plasmoddlum falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Li L.H., Li M., Wu Y.S., Wang P.;
Submitred (JUN-201) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12927; CAA73390.1; -
EMBL; AX040586; AAK77969.1; -
HSSP; P24295; IAUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99089647; PubMed-9874251;
Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,
Krauth-Siegel R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 AA; 52546 MW; 50A37C23484C387A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 FKRVADAMLAYG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 463 FTKVADAVKAQG 474
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                                            OPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRF 124
                                                                                          HPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRH 184
                                                                                                          ISYVQDVPAGDIGVGARRIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVL 244
                                                                                                                                                                                          FVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTRE 304
                                                                                                                                                                                                                                                                                          ELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLN 422
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                     57
64
               TGRFVVLDK-----NASNYESLV----DQEMNNVYERVMKLDPNQVEFLQAFHEILYSL
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                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.3%; Score 1265; DB 2; Length 442; 58.8%; Pred. No. 1.2e-80; ive 57; Mismatches 114; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P24295; JAUP.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006095; GLFV dehydrog.
FEan; PF00208; GLFV dehydrog. 1.
PFam; PF00208; GLFV dehydrog. 1.
PRINTS; PR00082; GLFV DEHYDROGENSE; 1.
PROSITE; PS0074; GLFV DEHYDROGENASE; 1.
SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCE4CC CRC64;
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STRAIN=FCQ 27;
Yuan P., Stewart T.S.;
Submitted (NAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF098675; AAD11789.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Glutamate dehydrogenase.
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Best Local Similarity 58.89
Matches 258; Conservative
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                                                               GKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLA
ORKNRCFRVQYNSALGPYKGGLRFHPSVNLSIVKFLGFEQIFKNSLTGLSMGGGKGGSDF
                                                                                                        LTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLE
                                                                                                                                                                KGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVGDRRKP
                                                                                                                                                                                                                              WELDCQVDIAFPCATQNEI DEHDAELLI KHGCQYVVEGANMPSTNEAIHKYNKAGI IYCP
                                               DPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGV
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AGANIAGFLKVAESYIEQG 440
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Job time: 87.1641 secs
                 99
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 8, 2005, 02:27:13; Search time 20.6536 Seconds (without alignments) 2217.496 Million cell updates/sec Run on:

US-10-627-886-26 2465 1 MDATTGDFTALQKAVKQMAT......GANIAGFTKVADAVKAQGAV 476 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	glutamate dehydrog							deh		fic	dehy	deh	ific			fic	deh	glutamate dehydrog	fic	NADP-specific glut	deh		glutamate dehydrog		glutamate dehydrog	glutamate dehydrog		glutamate dehydrog	glutamate dehydrog
SUMMARIES	S17949	A42489	H83072	H81050	B81825	A64053	T10487	D98019	H95151	E83912	E75362	DEECEN	F96990	C90937	G85785	A11503	832227	A33504	AF0710	A11144	AE0483	D64567	S22403	B95277	F71862	806938	DENCEN	S04904	. 809895
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Score	2444	1324.5	1309	1300.5	1294.5	1238	1214.5	1214	1212	1210.5	1205.5	1201	1199	1198	1198	1189.5	1185	1182	m	1180.5	1153	1150	1143	1142.5	1139	1133.5	1121.5	1115.5	1109
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51 2 741492 54 1 25275 54 1 25275 24 2 851960 24 2 896556 16 2 745284 116 2 745284 21 2 783852 24 2 A70055 26 2 669933 27 2 068923 20 2 075176 20 2 075176 20 2 784142 21 2 881079	44446444444444444444444444444444444444	probable glutamate	glutamate dehydrog	glutamate dehydrog	glutamate dehydrog	hypothetical prote	glutamate dehydrog	NAD-specific gluta	glutamate dehydrog								
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ALIGNMENTS

	RESULT 1		
	S17949 glutamate dehy N;Alternate na	S17949 glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment) Abliternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase	(fragment) 3e
	C;Date: 30-Jun	cella Bolokiniana 1922 #aquence revision 23-Mar-1995 #text_change 09-Jul-2004 0040. c170cn. c19030	
	R, Cock, J.M.;	R;Cock, J.M.; Kill, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R.	
	A; Title: A nuc	Figure NOI: 5101: 17, 1023-1044, 1991 A:Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADE	astic NADE
	A; Reference number: A; Accession: S17949	A;Kererence number: S17949; MULD:92032762; PMLD:1718478 A;Accession: S17949	
	A;Molecule type: DNA A:Regidues: 1-523 <coc></coc>	: DNA	
	A; Cross-refere	A; Cross-references: UNIPROT: P28998; EMBL: X58831	
	A; Accession: S17950 A; Molecule type: mRNA	1950 : mrnA	
	A;Residues: 1-523 <coc2></coc2>	23 <coc2></coc2>	
	A; Cross-releren R; Schmidt, R.R.	A;cross-rererences: EMBL:X58832; NID:g18272; FIDN:CAA41636.1; FID:g18273 R:Schmidt, R.R.	•
	submitted to t	submitted to the EMBL Data Library, April 1991	
	A;Reference number: S19030 A;Accession: S19030	Der: S19030 1030	
	A; Molecule typ	DNA	
	A; Residues: 1-	A;Residues: 1-219,'LW',222-523 <sch></sch>	
	A;Cross-referen	A;Cross-references: EMBL:X58831 C:Genetics:	
	A; Genome: nuclear		
	A;Introns: 6/2	A;Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; C:Sunerfamilv: clutamate dehydromenase (NAD(P)+)	,1; 272/2,
	C; Keywords: ch F; 202/Binding	C:Reywords: chloroplast; hexamer; NADP; oxidoreductase F;202/Binding site: substrate (Lys) #status predicted	
	Query Match	99.18;	
	Best Local Similarity Matches 472; Conserv	nifarity 99.2%; Fred. No. 1.2e-174; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
	Oy 1	1 MDATTGDFTALQKAVKQWATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 60	
	Db 48 1	48 MDATTGDFTALQXAVXQMATXAGTEGLVHGIXNPELRQLLTEIFMKDPEQQEFMQAVREV 107	
	Oy 61	AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120	
	υ ν το σ	AVSLQPVFEKRPELLPIFKQIVEPERVITPRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 167	
	Qy 121 (GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 180	
	Db 168	GERFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 227	
	Qy 181	LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY 240	
_	Db 228	LORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTGKGQEYGGSEIRPEATGY 287	

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Glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PAOI)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83072
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br addman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathchitisterence number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83072
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <STO>
A;Crose-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:g9950829; PIDM:AAG0797;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (straic) Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: Hando #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81050
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, N.D.; Dougherty, B.A.; Science 287, 1809-1815, 200,
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GKGGSDFDPKGKSDAEVWRFCQSFWSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 WLDDAGNLOVNRGPRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 5.7e-90; 55; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: gdhA; PA4588
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%; Score 1309;
59.2%; Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.29
Matches 263, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214
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NiAlternate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lambia

NiAlternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C;Species: Glardia lambia
C;Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A42489

R;Yee, J; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A;Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A;Reference number: A42489; MUID:92218410; PMID:155991
A;Reference number: A42489; MUID:92218410; PMID:155991
A;Residues: 1-449 <XES-
A;Cross-references: UNPROT:P28724; GB:M84604; NID:9159108; PIDN:AAA29155.1; PID:9159108
A;Note: sequence extracted from NCBI backbone (NCBIN:94074)
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase
F;125/Binding site: substrate (Lys) #status predicted
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288 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 347
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                                                                                                           FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNBIDEH 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 EFTGVLTGROVKWGGSFIRPEATGYGAVYFLEEMCKDNNTVIRGROVLLSGSGNVAQFAC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKS---DTAVYV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 EKLIQLGAKVLTF8DSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRYSEFKDKYPSVAYYE 304
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                                                                                                                                                                                 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                              216 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                             PTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATQNEIDEH
                                                                                                                                                                                                                                                                                       LNWTREEVROKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                  36 VROLLTEIPMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWL
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53.7%; Score 1324.5; DB 1; Length 449;

Best Local Similarity 58.2%; Pred. No. 4e-91;

Matches 260; Conservative 67; Mismatches 111; Indels 9;
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A;Recession: BB1825 A;Status: preliminary A;Molecule type: DNA A;Readidues: L-444 <ARR>
A;Recession: BB1825 A;Status: preliminary A;Molecule type: DNA A;Readidues: L-444 <ARR>
A;Recession: Ballata Source: serogroup A, strain Z2491
C;Genetics: A;Genetics: A;G
                                             A;Status: preliminary
A;Molecule: preliminary
A;Molecule: 1-444 <TET>
A;Crosd-references: UNIPROT:O9JY71; GB:AE002521; GB:AE002098; NID:g7226962; PIDN:AAF4205
A;Experimental source: serogroup B, strain MC58
C;Genetical Source: A;Genetical Source: Serogroup B, strain MC58
C;Genetical Source: Serogroup B, strain MC58
C;Genetical Source: MB1710
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 YFEKQKPWGV--AABIALPCATQNELDEBAAKTLLANGCYVVAEGANMPSTLGAVEQFIK 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGKGGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVROLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
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                                                                                                                                                                                                                                                                               Query Match 52.8%; Score 1300.5; DB 2; Length 444; Best Local Similarity 57.4%; Pred. No. 2.4e-89; Matches 257; Conservative 72; Mismatches 104; Indels 15;
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A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81050
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A;Accession: A64053
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-449 <TIGR>
A;Cross-references: UNIPROT:P43793; GB:U32704; GB:L42023; NID:g1573143; PIDN:AAC21858.1.
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase
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                                                                                                                                                                                                                                                            123 GGKGGSDFDPKGKSDAEVWRFCQAFWTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK 182
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92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL---PIFKQIVEPERVITFRV
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YVKGANVAGFMKVAKAMMAQG

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RESULT 7
T10487
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola
C; Species: Prevotella ruminicola
C; Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: T10487
R; Men. Z. T.; Morrison, M.
submitted to the EMBL Data Library, December 1996
A; Recession: T10487
A; Recession: T10487
A; Residues: prellminary; translated from GB/EMBL/DDBJ
A; Residues: 1-44 evERD.
A; Residues: 1-44 evERD.
A; Residues: 1-44 evERD.
A; Cross-references: UNIPROT: P95544; EMBL: U82240; NID: g1772844; PID: g1772845
A; Cross-references: UNIPROT: P95544; EMBL: U82240; NID: g1772845
C; Genetics:
A; Note: gdhA
C; Superfamily: glutamate dehydrogenase (NAD(P)+)
C; Keywords: NADP; oxidoreductase
                                                                                                                                                 | DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGK 155
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191 ACVFTGRGLSFGGSLIRPEATGYGLIYFAQAMLAEKGDSFAGKVVSVSGSGNVAQYAIEK 250
                                            LLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKKNNSARISEYKSDTAVYVGDRRK 337
                                                             251 ALSLGAKVVTCSDSSGYVYDPNGFTTEKLAALFDI-KNTKRGRVKDYAEQPGLQYPEGKR 309
                                                                                                                           PWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYC 397
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49.3%; Score 1214.5; DB 2; Length 444;
Best Local Similarity 54.9%; Pred. No. 6.5e-83;
Matches 242; Conservative 73; Mismatches 119; Indels 7;
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                                                                                                                                                                                                  Length 448;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                 Query Match
49.2%; Score 1214; DB 2;
Best Local Similarity 55.7%; Pred. No. 7.1e-83;
Matches 248; Conservative 62; Mismatches 127;
                                                                                                                                                               A;Gene: gdhA
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: oxidoreductase
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WADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: O:3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: H95151 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, G.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtrapple, Science 293, 498-506, 2001

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A, Map position: 1
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: H95151
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 «KUR»
A;Residues: 1-448 «KUR»
A;Cross-references: UNIPROT:097084; GB:AE005672; PIDN:AAK75409.1; PID:g14972791; GSPDB:GCGenetics:
C;Genetics:
A;Gene: SP1306
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MaDP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C-12 C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: E83312 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirra Naticle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MuID:20512582; PMID:11058132 A;Accession: E83312 A;Accession: E83312 A;Accession: E83312 A;Residues: 1-458 <STO>A;Accession: E83312 A;Cross-references: UNIPROT:09KB34; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB058 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                        Query Match 49.2%; Score 1212; DB 2; Best Local Similarity 55.5%; Pred. No. 1e-82; Matches 247; Conservative 63; Mismatches 127;
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C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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glittamate dehydrogenase - Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Oi-Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
CiAccession: E75362
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75362
A;Accession: E75362
A;Accession: B75362
A;Accession: DNA
A;Residues: 1-424 < WHI>
A;Residues: 1-424 < WHI>
A;Residues: 1-424 < WHI>
A;Residues: 1-424 < WHI>
A;Resperimental source: strain R1
C;Genetics:
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                                                                                                                        64 IVEPERVISFRVPWVDDQGNVQVNRGFRVQFNSALGPYKGGLRFHPSVNASIIKFLGFFQ 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMK 437
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                                                                                                                                                                                                                                                                                                                                                                                                    KRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKXNNSA
-MKDPEQQEFMQAVREVAVSLQPVFEKRPELL - - PI FKQ
                            141 IFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 MOAVREVAVSLOPVFEKRPELL - PIFKQIVEPERVITFRVSWLDDAGNLOVNRGFRVQY
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LVHGIKNPDVRQLLTEIF-
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NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum C; Species: C; Accession: F96990 C; Accession: F96990 C; Accession: F96990 C; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Closh, A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: F96590
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-443 < KURx
A; Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK78713.1; PID:g15023619; GSPDB:CCG; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 VLFAPGKAANAGGVATSGLEMAQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEOT 423
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                                                        127 GKGGSDPDFKGKSBGEVMRFCQALMTELYRHLGADTDVPAGDIGVGGREVGFMAGMMKKL
                                                                                                                                                                   4 LKHVMDDVIKRNPNEPEFHQAVKEVILSLEIVAEKHPEWVKDKIFDKIVEPERQIIFRVP
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                              GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
                                                                                                                                 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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Best Local Similarity 54.4%
Matches 242; Conservative
                                                                                                                                    214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRAP White dehydrogenase (NADP) (EC 1.4.1.4) - Escherichia coli (strain K-12)

N.Alternate names siglutamatic dehydrogenase; NADP-specific glutamate dehydrogenase
(S.Species: Escherichia coli
(S.Species: Escherichia 
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                                                                                                                                                                                                                352 ATONEIDEHDAELLIKHGCOYVVEGANMPSTNRAIHKYNKAGIIYCPGKAANAGGVAVSG 411
                                                                                                                                                                                                                                                                                                                           LEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRR--YNVDLAAGANIAGFTKVADA 469
                                                                                                                                                                                                                                                                                                                                                    94 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 QGYVYBPNGFTREQLQAVQDMKKKONSARISBYKSDTAVYVGDRRKPWELDCQVDIAFPC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GGTVVDEDGFTYDKLAVLMDIKNERR-GRVEDYAREVGAEFRPGVRPW--DVPVDVALPC
                                                                                                                                                                                                                                                  298 ATQNELGADDARTLIAGGVRVVAEGANMPCDLAAIQAFEEAGVLYAPGKATNAGGVATSG
EIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDS
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48.7%; Score 1201; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 6.6e-82;
Matches 241; Conservative 67; Mismatches 128; Indels 1
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C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: homohexamer; NADP; oxidoreductase
F;128/Binding site: substrate (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                VKAQGAV 476
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418 MREOGVL 424
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Cyaccession: G85785
R; Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhen iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Article: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: G85785
A; Status: preliminary
A; Molecule type: DNA
A
         C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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Cipecies: Escherichia coli
Cipecies: Escherichia coli
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
CiAcceshin. C90937
CiAcceshin. T: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H..
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend
A:Accession: C90337
A:Accession: C90337
A:Accession: C90337
A:Coss-references: L-447 - HAX>
A:Coss-references: thin O157:H7, substrain RIMD 0509952
C:Genetics: Ecs2467
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90937
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                                                          392 AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 451
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Best Local Similarity 53.8%; Pred. No. 1.1e-81;
Matches 240; Conservative 68; Mismatches 128;
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                                                                                                                                                                                452 VD--LAAGANIAGFTKVADAVKAQG 474
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RESULT 15 GBS785 MDP-specific glutamate dehydrogenase (imported) - Bscherichia coli (strain O157:H7, sub C;Species: Bscherichia coli

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246
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                                                                                                                   Gaps
                                                                                                                 10;
                                                                  Query Match
48.6%; Score 1198; DB 2; Length 4.
Best Local Similarity 53.8%; Pred. No. 1.1e-81;
Matches 240; Conservative 68; Mismatches 128; Indels
A;Gene: gdhA
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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Protein e Streptoco Enterococ

Protein e Protein e Streptoco Protein e S. pneumo E. faecal Bacterial Protein e Bacterial Protein e Glutamina

Adh97147 Aaba8636 Abb30172 Abp28423 Abp28423 Abu44405 Abu38946 Abu38946 Abu38946 Abu38946 Abu38946 Abu38946 Abu38946 Abu38946 Abu38946 Abu38346 Abu1740 Abu20218 Abu20218 Abu20218 Abu20218

AAU91467 AAB88356 ABB38536 ABB38536 ABB28423 ADH84405 ABU44405 ABU38946 ADK47974 ABU21749 ADS21354 ADN17964 ADN17964 ADN17964 ADN13354 ADN23354 ADN23354 ADN06095

E. faecal Haemophil Haemophil

Protein

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1 MDATTGDFTALQKAVKQMAT......GANIAGFTKVADAVKAQGAV 476
                                                                                                               2105692
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                   2105692 seqs, 386760381 residues
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                           protein search, using sw model
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ALIGNMENTS

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SUMMARIES

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Result Š Aaw15412 NADP-spec Aau98955 Mature NA Adq36731 Mature NA Aau98954 Mature NA Adq36729 Mature NA

Description

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subunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynuclectide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased tied, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chloralla sockiniana mature NADP-glutamate dehydrogenase beta subunit, used in the
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Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
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                                                                                                                                                                                    Claim 7; Page 31-32; 35pp; English.
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate debydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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                                                                                                                                                                                                                                                                                           NADP-specific glutamate dehydrogenase, NADP-GDH; alpha subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                           421 LINTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                        LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
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                                                                                                                                                                                                                                                           Mature NADP-glutamate dehydrogenase alpha subunit.
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                                                                                                                                              AAU98954 standard; protein; 487
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Matches 476; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Chlorella sorokiniana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCHM/) SCHMIDT R R. (MILL/) MILLER P.
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                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 26; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%;
Matches 476; Conservative 0
                                                                                     24-JUL-2003; 2003US-00627886
                                                                                                                         98US-00070844
                                                                                                                                                                                                                                                       2004-533134/51.
                                                                                                                                                              SCHMIDT R R.
                                                                                                                                                                                                                   Miller
                                                                                                                                                                                   (MILL/) MILLER P.
                                                                                                                                                                                                                                                                          N-PSDB; ADQ36730.
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                   US2004128710-A1
                                                                                                                         01-MAY-1998;
                                                                                                                                                                                                                   Schmidt RR,
                                                     01-JUL-2004
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sequence is the mature alpha subunit of the NADP-specific GDH used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
                                                                                                           0; Indels
                                                                            ; Score 2465; DB 8;
; Pred. No. 3.1e-228;
0; Mismatches 0;
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                                                                            100.0%;
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N-PSDB; AAT64530, AAT64543.
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                                                                                                          Matches 476; Conservative
                method of the invention.
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                                                                                             Local Similarity
                                               Sequence 487 AA;
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10-JUL-1997
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                                                                                                                                           360
                                                                                                                                                                      371
                                                                                                                                                                                                       420
                                                                            300
                                                                                                                                                                                                                                     431
                                                                                             252 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrogen metabolism; plant, glutamate dehydrogenase; GDH; enzyme;
alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having gluntamate dehydrogenase activity.
                                                                                                                                                           FTREQLQAVQDMKKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGGEYGGSEIRPEATGY
                                                                                                                                                                                                       DAELLI KHGCQYVVEGANMPSTNEA THKYNKAGI IYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                       GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                         FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATQNEIDEH
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                                                                                                                                                                                                                                                                                                 487
                                                                                                                                                                                                                                                                                    Mature NADP-specific GDH alpha subunit, SEQ ID 24.
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                                                                                                                                                                                                                                                                                                                                                                            ADQ36729 standard; protein; 487 AA
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N-PSDB; ADQ36728.
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2 Polypeptides (AAWIS407 and AAWIS408) respectively comprise the alpha (AAWIS407) and beta subunit (AAWIS408) precursor proteins of an ammoniuminducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAWIS411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by AAMIS4547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating departains (Updated on 17-OCT-2003 to standardise OS field)
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 DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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Pred. No. 3.4e-228;
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                                                                    Claim 1; Page 29-32; 61pp; English.
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynuclectide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella present sequence dehydrogenase beta subunit, used in the method
                                                                                                                                                                                                                                                                                        Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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Matches 476; Conservative
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               Chlorella sorokiniana.
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                                                                                                                                                                                                             Schmidt RR, Miller
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                                                                                                                                                               (SCHM/) SCHMIDT R (MILL/) MILLER P.
                                                                                                                                                                                                                                                          N-PSDB; ABK51008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention
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Claim 1; Page 25-27; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polypeptide having glutamate dehydrogenase (DDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36703), a beta subunit of NADP-specific GDH (ADQ36701), or their fragments, which exhibits GDH activity. The polypeptide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful from a polynucleotide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful control of the netholism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, commonic strees, and composition of the crop or plant. The present composition of the beta subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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                                                                                                                                                                                                                                          Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having gluntenate dehydrogenase activity.
457 LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 512
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                                                                                                                                                                                                      NADP-specific GDH beta subunit precursor protein, SEQ ID 4.
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                                                                                         ADQ36709 standard; protein; 512
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                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt RR, Miller P;
                                                                                                                                                                                                                                                                                                 Chlorella sorokiniana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCHM/) SCHMIDT R R. (MILL/) MILLER P.
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Matches 476; Conserv
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2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GPH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. inoreased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating:deaminating activity
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                                                      LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                       FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
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LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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Matches 476;
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ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
(Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                  GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCABLLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                           171 GLRFHPSVNLSIMKELAFBQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFWTE
                                                                           1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                     DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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                                                            Gaps
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                                           Length 526;
                                                          Indels
                                        100.0%; Score 2465; DB 2;
llarity 100.0%; Pred. No. 3.5e-228;
Conservative 0; Mismatches 0;
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                                                 Similarity
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                         Sequence 526
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Best Local Simi:
Matches 476; (
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate debydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the
Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
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100.0%; Pred. No. 3.5e-228;
iive 0; Mismatches 0;
                                                                                                                                                               Claim 6; Page 13-15; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 526 AA
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121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 180
  LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ratios (i.e. higher capacity for glutamate synth (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                Chlorella sorokiniana; strain UTEX 1230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 44-46; 61pp; English.
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                                                                                                                                  AAW15411 standard; protein; 487
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(first entry)
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N-PSDB; AAT64547.
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10-JUL-1997
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Matches 475;
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AAW15411
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                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polypeptide having glutamate dehydrogenase (DDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36703), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen method is niplant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmocic stress, and composition of the crop or plant. The present osmocic stress, and composition of the crop or plant. The present osmocic stress, and composition of the alpha subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
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                                                                                                                                                                                                                                                                                     assing or decreasing nitrogen metabolism in plant cells, for pla increased yield and improved tolerance to ammonia toxicity and its stress, by transforming plant cell with nucleic acid having
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; SEQ ID NO 2; 36pp; English.
                                                                                                                                                                                                                                                                                                                                              glutamate dehydrogenase activity.
                                                                                          98US-00070844.
                                                    24-JUL-2003, 2003US-00627886
                                                                                                                                                                                       Schmidt RR, Miller P;
                                                                                                                            (SCHM/) SCHMIDT R R. (MILL/) MILLER P.
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N-PSDB; ADQ36706.
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              01-JUL-2004
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2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isonarymaes of Chlorella sorokiniana. They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (pref. increasing them sasimilation of inorganic N into organic N) by transforming them with nucleoride sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating ideaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 MDATTGDFTALQKAVKQWATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism; chloroplast; transgenic plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADP-specific glutamate dehydrogenase alpha subunit.
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251
                                                                                                                                                                                FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEQ 371
                                                                                                                                                                                                                                         DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 431
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                       GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                     GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                               PTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                            LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                          DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                               LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGGEYGGSEIRPEATGY
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #24290.
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
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Trawick JD,
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N-PSDB; ACA42633.
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proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. sureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of cut organism in cells other than S. aureus, S. typhimurium, cell the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the formula process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%; Score 1309; DB 6;
59.2%; Pred. No. 8.2e-117;
iive 55; Mismatches 120;
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Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 445 AA;
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The invention relates to a novel composition comprising outer-membrane vesicles (OWV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OWVs prepared from a second strain of N. meningitidis, but which are not present in OWVs prepared from the first strain. The composition of the invention demonstrates antibacterial and antinifammatory activities and may be useful in the field of meningococcal blochemistry, in particular the trafficking and localisation of meningococcal proteins, as well as in the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MCS8 outer-membrane vesicle (OWV)-related membrane protein
New compositions having outer-membrane vesicles and proteins from
Neisseria meningitidis, useful in the field of meningococcal
blochemistry, in particular for preventing and/or treating meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
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                                                                                                                                                                                                                                                                                                                                                                                                        meningococcal protein trafficking; localisation; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis MC58 OMV-related membrane protein -
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                                                                                                                                                                                                                                                                                                                                                                                    outer-membrane vesicle; antibacterial; antiinflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.8%; Score 1300.5; DB 8; ilarity 57.4%; Pred. No. 5.4e-116; Conservative 72; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 163; 79pp; English
                                                                 453 DLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                ADP08330 standard; protein; 444 AA
                                                                                         15-NOV-2002; 2002GB-00026734.
27-MAR-2003; 2003GB-00007131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2003; 2003WO-IB006281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis MC58.
                                                                                                                                                                                                                                                                                                 26-AUG-2004 (first entry)
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                                                                                                      427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa equences or other sequences of pseudomonas species using biochip technology. Sequences ABG67836-ABG8436 represent P. aeruginosa phycptides of the invention Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV 452
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59.2%; Pred. No. 8.3e-117;
ive 55; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 20646; 455pp; English
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                                                                                                                                                                                                                                                       THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html
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98US-0094190P.
                                                                                                                                                  99US-00252991
                                                                                                                                                                                                                                                                                            Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263; Conservative
                        Pseudomonas aeruginosa
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Best Local Similarity
Matches 263; Conserv
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                                                                                                                                                                                                                                                       GENO-) GENOME
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                                                             US6551795-B1
                                                                                                                                                  18-FEB-1999;
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                                                                                                                                                                                                                                                                                      1 MAVSLEEQISAMDATTGDFT......GANIAGFTKVADAVKAQGAV 487
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-070-844-4
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6 US-10-627-886-2
US-09-070-844-26
6 US-10-627-886-26
5 US-10-282-122A-66687
8 US-10-288-943-43
5 US-10-282-122A-65129
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 66041, Ap Sequence 152, App Sequence 1341, Ap Sequence 1341, Ap Sequence 45200, A Sequence 3131, App Sequence 58056, A Sequence 58056, A Sequence 66870, A Sequence 66870, A Sequence 61739, App Sequence 6171, App Sequence 6171, App Sequence 6171, App Sequence 6171, App Sequence 611, App	POLYNUCLEOTIDES -SUBUNITS OF GLUTAMATE (ODS OF USE #1.25
US-10-282-122A-66041 US-10-275-026A-152 US-10-369-493-13947 US-10-369-493-9839 US-10-369-493-9839 US-10-282-122A-45200 US-10-282-122A-45200 US-10-282-122A-57310 US-10-282-122A-57310 US-10-282-122A-72329 US-10-282-122A-72329 US-10-282-122A-74024 US-10-282-122A-74024 US-10-282-122A-74024 US-10-369-493-617 US-10-369-493-617 US-10-369-493-617 US-10-369-493-8215 US-10-369-493-8215 US-10-369-493-10621 US-10-369-493-10621 US-10-369-493-10621 US-10-369-493-10621 US-10-369-493-10621 US-10-369-493-10621 US-10-282-122A-53198 US-10-282-122A-53998 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82 US-11-073-550-82	ALIGNMENTS 44 PEPTIDES AND ASES AND METH iwanchik t, Suite A-1 L.0, Version 0,844 96
44444991155 44444991155 44444991155 44444991155 44444991155 44444991155 44444991155 44444991155 444449991155 444449991155 444499991155 444499991155 444499991155 444499991155 444499991155	on US/0907084 95A1 , Robert R. Philip NOVEL POLYP RELATING TO DEHYDROGENA : 26 ESS: anchik & Sali . 41st Street e Compatible PC-DOS/MS-D IN Release #1 DATA: R: US/09/070 ATA: R: US/09/070
00000000000000000000000000000000000000	HULT 1 109-070-844-24 Gequence 24, Application US/090708 Vatent No. US2002062495A1 GENERAL INFORMATION: APPLICANT: Miller, Philip TITLE OF INVENTION: NOVEL POLY TITLE OF INVENTION: DEHYDROGEN TORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanchik & Sal STRET: 2421 N.W. 41st Stree CITY: Gainesville STRATE: Florida COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Florpy disk COMPUTER: IBM PC COMPATA: MEDIUM TYPE: Ploppy disk COMPUTER: PATENTION DATA: APPLICATION NUMBER: US/09/07 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/09/07 FILING DATE: REGISTRATION NUMBER: 36,965 REFERENCE/DOCKET NUMBER: UF!
1294.5 1294.5 1287.5 1287.5 1289.5 1239.5 1230.5 1230.5 1230.5 1230.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 1200.5 12	1 100-844- TICE 24, TICE OF TICE OF TI
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100.0%; Pred. No. 3.9e-218;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                              NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                    APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-0CT-95
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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US-09-070-844-4
; Sequence 4, Application US/09070844
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Best Local Similarity 100.0
Matches 487; Conservative
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Miller, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
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                                                                                                                                                                                                                        Length 487;
                                                                                                                                                                                                                                                           Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: dainesville
STATE: Florida
COUNRY: USA
ZIP: 3260-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
                                                                                                                                                                                                                    100.0%; Score 2513; DB 9;
100.0%; Pred. No. 3.9e-218;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/10627886 Publication No. US20040128710A1 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-8000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGITH: 487 amino acids
TYPE: amino acids
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Best Local Similarity 100.
Matches 487; Conservative
                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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US-10-627-886-24
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                                                                                                                                                                                                                          Sequence 4, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: ROVEL POLYPEPTIDES AND POLYNUCLEOTIDES
BERYPROGENASES AND SUBUNITS OF GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%; Score 2508; DB 16; Length 512; 100.0%; Pred. No. 1.2e-217; tive 0; Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/627, 886
FILING DATE: 24-Jul-2003
CLASSIFICATION NUMBER: 09/70, 844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 09/725, 596
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725, 596
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISCHARTON NUMBER: 35, 589
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REFERENCE/DOCKET NUMBER: 35, 589
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 512 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 486;
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US-10-627-886-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DEHYDROGENASES AND SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
CITY: Gainesville
STATE: Ploxida
CUNTRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AVSLEBQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/725,596

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REFERENCE/DOCKET NUMBER: 36,965

REFERENCE/OCKET NUMBER: 196,95

TELECOMMUNICATION INFORMATION:

TELECHOME: (904) 372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUINCE CHARACTERISTICS:

LEMETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2e-217;
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99.8%; Score 2508; L
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 486; Conservative 0; Mismatches
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amino acid
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99.8%; Score 2508; DB 9; I
100.0%; Pred. No. 1.2e-217;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-011-2003
CLIASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAX-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  Query Match
Best Local Similarity 100.
Matches 486; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAQGAV 487
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US-10-627-886-2
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Jeant No. US20020062495A1

Jeant No. USCONTING: Philip

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                                                                                                                                                                                                                                                                                           302 SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
YSSAIGPYKGGIRFHPSVNLSIMKFLAPEQIFKNSLTTLPMGGGKGSBDPDFKGKSDAEV
                                                                                                               207 MRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTFKGQEYGG
                                                                                                                                                                                                                       267 SEIRPEATGYGAVLFVENVLKÖKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                                                                                                                                                                                                                                                                                                            327 SQGYVYEPNGFTREQLQAVQDMKKKNNSARISBYKSDTAVYVGDRRKPWELDCQVDIAFP
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                                                                                 MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
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CLASSIFICATION:
PRIOR APPLICATION
APPLICATION UNBER: 08/725,596
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET UNBER: UF155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 526 amino acids
amino acid
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MOLECULE TYPE: protein
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; Publication No. US20040128710A1
; GENERAL INFORMATION:
    APPLICANT: Schmidt, Robert R.
    APPLICANT: Schmidt, Robert R.
    TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
    TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                  GLEMIQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                                                                                                                                                          QEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ
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                                                                                                                2 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
                                                         Gaps
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Length 526;
                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
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61 AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVLFVENVLKÖKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
98.1%; Score 2465; DB 9; L
Best Local Similarity 100.0%; Pred. No. 8.3e-214;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                           Version #1.25
                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPICATION:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-10-627-886-26
; Sequence 26, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-070-844-26
      Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AVSLERQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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Patent No. US20020062495A1

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: BEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                     Length 526;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 2508; DB 16;
100.0%; Pred. No. 1.2e-217;
ive 0; Mismatches 0;
                                                      NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELEPHONE: (352) 375-8100
TELEPAK: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 486; Conservative
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US-09-070-844-26
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Gaps

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APPLICANT: Trawlex, John
APPLICANT: Trawlex, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT PILLING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/201, 27
PRIOR APPLICATION NUMBER: 60/200, 848
PRIOR APPLICATION NUMBER: 60/200, 347
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-26
                                  DAELLIKHGCÇYVVEGANMPSTINEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 420
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     DABLLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                               LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 487
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                                                                                                                                                                                                                                                                                                        Sequence 66687, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66687
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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SEQ ID NO 66687
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Best Local Similarity 59.2%;
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind, Judith
Wall, Daniel
Trawick, John
                                                         361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AVSLQPVPEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 LORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFPCATQNEIDEH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH 360
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                            Miller, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
ELATING TO THE .- AND -SUBUNI'S OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN POC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver
SOFTWARE: PACENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAX-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 01-MAX-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/725,596
APPLICATION NUMBER: 08/541,033
FILING DATE: 03-OCT-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lloyd, Jeff
REGLSTRATION NUMBER: 35,589
REPERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEFANNE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-627-886-26
APPLICANT: Schmidt, Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                               CITY: Gainesville
STATE: Florida
COUNTRY: USA
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APPLICANT: AL, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR PELICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/203,335

PRIOR PELICATION NUMBER: 60/230,335

PRIOR PELICATION NUMBER: 60/230,335

PRIOR PELING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,337

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2001-02-10

PRIOR PELING DATE: 2001-02-10
       360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG 415
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                                                             485
                                                                                           462 ----NVDLAAGANIAGFTKVADAVKAQG
                                                                                                                                                                                                                           ; Sequence 65129, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129
                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
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Yamamoto, Robert
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                                                                                                                                                                                                      US-10-282-122A-65129
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Publication No. US20050176085A1
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: DENTIFICATION PEPTIDE ISOLATION FOR THE
TITLE OF INVENTION: DENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
TITLE OF INVENTION: COMPLEX MIXTURES.
FILE REFERENCE: Proteomics CU203-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT FILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
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                                                        284
                                                                                                                                              285 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 344
                                                                                                                                                                             245 AARKVWEMGGKVISLSDSBGTLYAEAGLSDEQWEYLMELKNVRR-GRIREWAEQFSLQFL 303
                                                                                                                                                                                                                                                       404
                                                                                                                                                                                                                                                                           304 EGRRPWGLAC--DIALPCATQNELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG 361
                                                                                                                                                                                                                                                                                                                                                405 IIYCPGKAANAGGVAVSGLEMTQNRMSLAWTREEVRDKLERIMKDIYDSA-MGPSRRYNV 463
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LENGTH: 444
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                                                       DVRQLLTBIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
                                                                                                3 DINTLFANLKORNPNOEPFHOAVEEVPMSLDPFLAKNPKYTOOSLLERIVBPERVOMFRV
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; Sequence 152, Application US/10275026A
; Publication No. US20040087770A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Christoph
; TILLE OF INVENTION: Virulence Genes, Proteins, and Their Use
; PILE REFERENCE: GJE-6436
; CURRENT APPLICATION NUMBER: US/10/275,026A
; CURRENT FILING DATE: 2003-10-31
; PRIOR PILING DATE: 2001-05-08
; PRIOR PILING DATE: 20001-05-08
; PRIOR PILING DATE: 2000-05-08
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72; Mismatches 105; Indels
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; ORGANISM: Neisseria meningitidis
US-10-275-026A-152
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 152
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Matches 256; Conservative
Matches 256; Conservative
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                                     183 IRNEFTSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
                                                                                                                  284 YCAELLLEKGAIVLSLSDSQGYVYEPN-GFTREQLQAVQDMKKKNNSARISEYKSDTAVY 342
                                                                                                                                                 243 YAABKAIQLGAKVLIVSDSDGFVLFPDIGMTBAQLAALIELKEVRRE-RVATYAKEGGLQ 301
                                                                                                                                                                                                                                     343 VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
                                                                                                                                                                                                                                                                    302 YFENQKPWGV--AAEIALPCATQNELDBEAAKTLLANGCYVVAEGANMPSTLGAVEQPIK 359
                                                                                                                                                                                                                                                                                                                                                           403 AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 461
224 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 283
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-20

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PPLICATION NUMBER: 60/230,335

PRIOR PPLICATION NUMBER: 60/230,337

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2000-12-22

PRIOR PPLICATION NUMBER: 60/267,636

PRIOR PLING DATE: 2001-02-09

PRIOR PPLICATION NUMBER: 60/267,636

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 ----NVDLAAGANIAGFTKVADAVKAQG 485
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US-10-282-122A-66041
Sequence 66041, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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SEQ ID NO 66041
LENGTH: 444
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Forsyth, R.
Xu, H.
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Best Local Similarity
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APPLICANT:
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Publication No. US20030233675A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: DAMYS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2000-02-21
FRIOR FILING DATE: 2000-02-21
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                                                                                                                                                                                      68 WYDDQGKVQYNRGYRIQMSSAIGPYKGGLRPHPSVNLSVLKFLAFEQVFKNSLTSLPMGG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 ILYAPGKASNAGGVAVSGLEMSONAMRLIWTAGEVDSKCHNIMOSIHHACVHYGEEADGR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 WLDDAGNLOVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 164
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                                                                                     8 VDNFLARLKORDPGOPEFHOAVEEVLRTLWPFLEANPHYLOSGILERMVEPERAVLPRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 VROLLTEIFMXDPEQOEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VESFLARLKKRDPDQPEFHQAVEEVLRSLWPFLEANPHYLTSGILERICEPERAVVFRVS
                                                       VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVPEKRPELLP--IFKQIVEPERVITFRVS
                                                                                                                                                          WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
     Gaps
     7;
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     Mismatches 124; Indels
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58.1%; Pred. No. 9.4e-107;
iive 59; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 VDLAAGANIAGFTKVADAVKAQGAV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Pseudomonas fluorescens
     55;
  259; Conservative
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SEQ ID NO 13947
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                                                                                                                                 243 YAAEKAIQLGAKVLIVSDSNGFVLFPDSGMSEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
                                                                                                                                                                                                         VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
                                                                                                                                                                                                                                          ::|||:::|| |:::| |:::| |:::| |:::| |:::| |:::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |:::::| |::::| |:::::| |:::::| |:::::| |:::::| |:::::| |:::::| |:::::| |:::::| |:::::| |:::::| |::::| |:::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |:::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| |::::| 
                                                                                                                                                                                                                                                                                                                  AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 461
ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
                              Score 1287.5; DB 15; Length 449; Pred. No. 2.5e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVGDTVNYVNGANIAGFVKVADAMLAQG 443
                                                                                                                                                                                                                                                                                                                                                                                                                          ----NVDLAAGANIAGFTKVADAVKAQG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67538, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%;
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Search completed: September 8, 2005, 02:38:55 Job time : 92.1268 secs

12638, A 2, Appli 6130, Ap 13935, A

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Sequence 1153, Applequence 23, Appledquence 32, Appledquence 7622, Applequence 7623, Appledquence 17482, Applemence 21, Appligedquence 2, Appli

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22, Appl 20, Appl 1153, Ap 23, Appl 832, Appl

Title: Perfect score:

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Sequence 24, Application US/08541033A

Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2513; DB 2; Length 487; 100.0%; Pred. No. 4.1e-223; ive 0; Mismatches 0; Indels 0
US-09-239-303-9
US-09-902-540-12638
US-09-328-352-6130
US-09-3489-039A-13935
US-09-489-039A-13935
US-08-461-990B-22
US-08-461-990B-22
US-09-538-092-1153
US-09-538-092-1153
US-09-949-016-7622
US-09-949-016-7622
US-09-949-016-7622
US-09-949-016-7622
US-09-949-016-7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAILIOCK, TED W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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Sequence 6537, Ap
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Sequence 26, Appl
Sequence 20446, A
Sequence 3884, Ap
Sequence 4489, Ap
Sequence 11, Appl
Sequence 11, Appl
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Sequence 4, Appli
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Sequence 2, Appli
                                                                                                                                                                                                             September 8, 2005, 02:01:27; Search time 26.0834 Seconds (without alignments) 1393.764 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-828-451-4
US-08-828-451-2
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US-08-828-451-2
US-08-828-451-26
US-09-252-91A-20646
US-09-38-352-5725
US-09-88-110-4489
US-08-88-640-3
US-08-88-640-3
US-08-88-640-3
US-08-370-193A-11
US-08-548-618-657
US-09-543-61A-6557
US-08-508-7618-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2513
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Match Length
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Database :

9

Gaps

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MAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPE 60

MAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPE

Matches 487; Conservative

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Sequence 767, App Sequence 4041, App Sequence 17483, A Sequence 3103, Ap

1147 1143 1037.5 1012 788.5 552.5 537.5

Result Š. Sequence 2162, Ap Sequence 11352, A

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                      linear
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                    TOPOLOGY:
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QQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRV 120
                    61 QQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRV 120
                                                               121 QYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAE 180
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Fatent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
ITILE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
CORRESPONDENCES:
ADDRESSEE: SALiwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
CONTENT: Florida
CONTENT: PLORIDA
                                                                                                                                                                                                                   241 GSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLS
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                                                                                                                                181 VMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Perentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: MILLIOCK, TED W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECHOMICATION INFORMATION:
TELEPHONE: (904) 372-5800
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OP SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Ploxida
COUNTRY: USA
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COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                  Score 2513; DB 2;
Pred. No. 4.1e-223;
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0
                                                         100.0%; Scc. No. 4.1.00.0%; Pred. No. 4.1.
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                                                                                                        Best Local Similarity 100.
Matches 487; Conservative
, MOLECULE TYPE: protein US-08-828-451-24
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TOPOLOGY:
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US-08-541-033A-2
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APPLICANT: Schmidt, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: BEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                   99.8%; Score 2508; DB 2; Length 512;
100.0%; Pred. No. 1.3e-222;
vative 0; Mismatches 0; Indels
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION WUNBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
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Patent No. 5985634
GENERAL INFORMATION:
                                                                                                                                                                                                     Query Match 99.8
Best Local Similarity 100.
Matches 486; Conservative
                                                                                                                                                                                      MOLECULE TYPE: protein
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STATE: Florida
COUNTRY: USA
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147 YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 CATQNEIDEHDAELLIKHGCQYVVGGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 GLEMTQNEMSLAWTREEVRDKLERIMKDIYDSAMGBSRRYNVDLAAGANIAGFTKVADAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.3e-222;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%; Score 2508; DB 2;
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08541033A Patent No. 5879941
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INPORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 512 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 486; Conservative
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SEIRPEATGYGAVLFVENVLKÖKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRICE APPLICATION:
PRICE APPLICATION:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whithock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMULICATION INFORMATION:
MARCISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 377-68100
TELERENOME: 6043,375-8100
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100.0%; Pred. No. 1.3e-222;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 486; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                            521 KAOGAV 526
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GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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99.8%; Score 2508; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 486; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WALLIOCK, TED W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFIS:
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
TELEFAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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RESULT 6
US-08=28-451-2
US-08=28-451-2
| Sequence 2, Application US/08828451
| Patent No. 598534
| GENERAL INFORMATION:
| APPLICANT: Schmidt, Robert R. APPLICANT: Miller, Philip
| TILLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
| TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS: 26
| ADDRESSEE: Saliwanchik & Saliwanchik | STREET: 2421 N.W. 41st Street, Suite A-1
| CITY: Gainesville | STATE: Florida | STATE: Plorida |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRFCQSFWIELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEFMQAVREVAVSLQPVPEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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301 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH 360
                                                                                                                                                                                                                                                                                                                            DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 431
                             241 GAVLFVENVLKOKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                          361 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
      132 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                             181 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKAYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                  GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                PTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                    LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPBATGY
                                                                                                                                                                                                                                                                                                                                                                                                               LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08828451
Sequence 26, Application US/08828451
Setent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: MILLS PHILIP
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.1%; Score 2465; DB 2; I
100.0%; Pred. No. 1.1e-218;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFRENCE/POCKET NUMBER: UP15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 476 amino acida
TYPE: amino acid
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Best Local Similarity 100.
Matches 476; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-828-451-26
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US-08-828-451-26
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SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 340
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                                                                                                                    CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                                             SQGYVYEPNGFTREQLOAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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98.1%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e-218;
Matches 476; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTAL: USANGE TO THE COUNTALL STATES OF THE COMPUTER LEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
RESISTANTION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
STATE: Plorida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/08541033A Patent No. 5879941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
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Sequence 5725, Application US/09328352
Facent No. 6562958
GENERAL INFORMATION:
TITLE GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 MPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKRCLVSGAGNVAQYCAELLLEKGALVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNS 329
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SNQFTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
                                                     285 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
                                                                                                                                                                                                                  250 AARKVWEWGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL
                                                                                                                          345 DRRKFWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                              IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 GKTVSISGSGNVAQYAAEKAMFIGAKVVTLSDSNGTVYLKNGFTDELLAEVMELKNIKR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 1257.5; DB 4; 55.9%; Pred. No. 2.6e-107; iive 61; Mismatches 128;
                                                                                                                                                                                                                                                                   464 DLAAGANIAGFTKVADAVKAQGAV 487
                                                                                                                                                                                                                                                                                        ORGANISM: Acinetobacter baumannii
US-09-328-352-5725
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Best Local Similarity 55.9
Matches 256; Conservative
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US-09-328-352-5725
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                     9
                  71
                                      GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                                                                                     GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                               LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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                                                                                      AVSLOPVPEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLOVNRGFRVQYSSAIGPYKG
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;; Pred. No. 4.4e-112;
55; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20646
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Matches 263, Conservative
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US-09-252-991A-20646
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APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, Maria V
APPLICANT: Lightfoot, Maria V
ATILE OF INVENTION: PLANTS CONTAINING THE GDA GE
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                    48.6%; Score 1221; DB 4;
55.7%; Pred. No. 5.7e-104;
iive 64; Mismatches 125;
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PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4489
LENGTH: 448
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,640
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4489
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Patent No. 5998700
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.7%
Matches 248; Conservative
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OP INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
                                                                                                                                                                                                            APPLICATE: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT APPLICATION NUMBER: US 60/055,778 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-06-15 NUMBER OF SEQ 1D NOS: 6812 SOFTWARE: Patent In version 3.1
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                                                                                                                          Sequence 3884, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
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US-09-583-110-4489
Sequence 4489, Application US/09583110
Patent No. 6699703; GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
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                                                                RESULT 11
US-09-134-000C-3884
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LENGTH: 448
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Best Local
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285 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 VROLLTBIFMKDPEQQBFMQAVREVAVSLQPVFBKRPBL--LPIFKQIVBPERVITFRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSUJIMOTO, NOBUHARU
APPLICANT: TSUJIMOTO, NOBUHARU
APPLICANT: TSUJIMOTO, NOBUHARU
APPLICANT: MISUJI KAZUHIKO
APPLICANT: MISUJI KAZUHIKO
TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
TITLE OF INVENTION: L-GLUTAMIC ACID BY FERMENTATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
47.8%; Score 1201; DB 3; Length 4
Best Local Similarity 54.0%; Pred. No. 4e-102;
Matches 241; Conservative 67; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 NVDLAAGANIAGFTKVADAVKAQGAV 487
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,235
FILING DATE: 27-UN-1997
CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEBNETH: 447 residues
TYPE: amino acid
STRANDEDNESS: not relevant
D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
VS-08-370-193A-11
Sequence 11, Application US/08370193A
; Patent No. 5573945
                                                                                                                                             PC-DOS/MS-DOS
                                     ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                       SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-884-235-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.8%; Score 1201; DB 2; Length 4. Best Local Similarity 54.0%; Pred. No. 4e-102; Matches 241; Conservative 67; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lightfoot, David A.
APPLICANT: Lightfoot, David A.
APPLICANT: Lightfoot, Mria E. Vidal
APPLICANT: Lightfoot, Mria E. Vidal
TITLE OF INVENTION: PLANTS CONTAINING THE gdha GENE AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SUCHENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Pillabury Madison E. Sutro, L.L.P.
STREET: LION New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 NVDLAAGANIAGFTKVADAVKAQGAV 487
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            CLASSIPCATION 900

PRIOR APPLICATION 1900

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,058

FILING DATE: 02-UL-1996

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIA, PAUL K.
REFERENCE/DOCKET NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 91163/24

TELEPHONE: (202)-861-3503

TELEPHONE: (202)-861-3503

TELEPAX: (202)-861-3503

TELEPAX: (202)-861-3503

TELEPAX: (202)-861-3503

TELEPAX: (202)-861-3503

TELEPAX: (202)-861-3603

SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids

TYPE: amino acid

TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-886-640-3
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165 GKGGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 224
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P. 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                     COMPUTER LOSA

ZIP: 2202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NOWBER: US/08/370,193A
FILING DATE: 09-74N-1995
CLASSIFICATION NOWBER: US/08/370,193A
FILING DATE: 09-74N-1995
CTASSIFICATION NOWBER: 10-714-0
TELEFRATION NOWBER: 10-714-0
TELEFRACOMMUNICATION INFORMATION:
TELEFRAX: 703-413-220
TELEFRAX: 703-413-220
TELEFRAX: 703-413-220
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TELEFRAX: 703-413-220
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TELEFRAX: 703-413-200
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47.8%; Score 1200; DB 1; 3
Best Local Similarity 54.0%; Pred. No. 4.9e-102;
Matches 241; Conservative 67; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 NVDLAAGANIAGFTKVADAVKAQGAV 487
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Search completed: September 8, 2005, 02:12:07 Job time : 27.0834 secs

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GenCore version 5.1.6
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odel	September 8, 2005, 02:12:18; Search time 88.1553 Seconds (without alignments) 2828.902 Million cell updates/sec	
ш ма би	05, 02:	
ch, usi	8, 20	-886-24
rotein sear	September	US-10-627-886-24 2513
OM protein - protein search, using sw model	Run on:	Title: US-10-627-886-24 Perfect score: 2513

Sequence: 1 MAVSLEEQISAMDATTGDFT......GANIAGFTKVADAVKAQGAV 487
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt 03:*

SUMMARIES

	tion	chlorella s	plasmodium	plasmodium	spironucleu	giardia lam	giardia lam	pseudomonas						pseudomonas	trichomonas				plasmodium		ruminococcu	acinetobact	clostridium	streptococc	enterococcu	haemophilus	streptococc	trypanosoma	mannheimia	streptococc	pasteurella	bacteroides
	Description	P28998	Q8ilf7	Q7rq39	07yzn9	Q7r3n7	P28724	Q9hvj7	09jy71	09jt56	088923	096940	QBilto	Q9z3c4	Q7yzu7	Q9tx88	Q9gtk5	Q68143	Q7rgt5	Q8g610	Q8ge72	Q6fd67	Q8xk85	Q8e4j6	Q835g2	P43793	08dyy7	061083	Q65w57	Q8dul2	Q9cpj4	P94598
SUMMAKIES	ID	DHE4 CHLSO	Q8ILF7	Q7RQ39	Q7YZU9	Q7R3N7	DHE4 GIALA	Q9HV <u>J</u> 7	Q9JY71	Q9JT56	088023	096940	QBILTO	Q9Z3C4	Q7YZU7	Q9TXS8	Q9GTK5	Q6SI43	Q7RGT5	Q8G6L0	Q8GE72	Q6FD67	Q8XK85	Q8E4J6	Q835G2	DHE4_HAEIN	Q8DYY7	061083	Q65W57	QSDUL2	Q9CPJ4	DHE3_BACTN
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	Query Match Length DB	523	510	1203	446	449	449	445	444	444	449	470	470	445	437	442	442	465	536	448	455	447	448	449	448	449	449	447	462	449	449	444
de	Query Match	97.3	54.7	54.2	52.8	52.8	52.7	52.1	51.8	51.5	51.2	51.2	51.2	51.1	51.1	50.3	50.3	50.0	49.9	49.8	49.8	49.7	49.4	49.4	49.3	49.3	49.2	49.1	49.0	49.0	48.9	48.8
	Score	2446	1375	1361	1328	1327.5	1324.5	1309	1300.5	1294.5	1287.5	1286.5	1286.5	1285	1284.5	1265	1264	1257	1253.5	1250.5	1250.5	1249.5	1241.5	1240.5	1239.5	1238	1236.5	1234	1231.5	1230.5	1230	1225.5
	Result No.	-	63	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	P95544 prevotella	Q8dpg0 streptococc	Q97qb4 streptococc	Q9kb34 bacillus ha	Q7vsn6 bordetella	Q9rtn9 deinococcus	Q64q81 bacteroides	Q7weu7 bordetella	Q88xm9 lactobacill	P00370 escherichia			Q97129 clostridium	
Q9AIW1	DHE4 PRERU	Q8DPG0	Q97QB4	Q9KB34	Q7VSN6	Q9RTN9	064081	Q7WEU7	Q88XM9	DHE4 ECOLI	966090	Q6AJB1	Q97L29	
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448	444	448	448	458	447	424	444	464	448	447	446	449	443	
48.7	48.3	48.3	48.2	48.2	48.0	48.0	48.0	48.0	47.8	47.8	47.8	47.8	47.7	
1225	1214.5	1214	1212	1210.5	1206.5	1205.5	1205.5	1205.5	1202	1201	1200.5	1200	1199	
32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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RESULT.

DIREA CHILSO

AC PARADARD; PRT; 523 AA.

AC PARADAR CHILSO

DIREA CHILSO

OL-DEC-1992 (Rel. 14) Last sequence update)

DIA DIREA CHILSO

OL DEC-1992 (Rel. 44) Last sequence update)

DIA DIREA CHILSO

OL DEC-1992 (Rel. 43) Last sequence update)

OS MADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)

OS MADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH)

CHOOTEL TAXID-3076;

RA COCK J.M. Kim K.D., Millor P.W. Hutson R.G., Schmidt R.R.;

RA DIA MADISTALIC ACTIVITY L. Glutamate H H(2)O + NADP(+) = 2-oxoglutarate chorophastic NADP-specific glutamate dehydrogenase (s) in Chlorella chorophastic NADP-specific glutamate H H(2)O + NADP(+) = 2-oxoglutarate chorophastic NADP-specific glutamate dehydrogenase (s) in Chlorella chorophastic NADP-specific glutamate H(2)O + NADP(+) = 2-oxoglutarate chorophastic NADP-specific glutamate H(2)O + NADP(+) = 2-oxoglutarate chorophastic NADP-specific glutamate dehydrogenase family.

CC - SUBDMITS are encoded by the same gene.

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                                                                                                                                                                                               38 AKRLRSRSPRMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPELRQLLTEIFMKDPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 158 YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
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                                                                                                                                   2 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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          Length 523;
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Plasmodium faTciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
   Score 2446; DB 1;
Pred. No. 3.9e-161;
3; Mismatches 9;
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog.
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EMBL; AE014820; AAN36899.1; -.
HSSP; P24295; IAUP.
Query Match
Best Local Similarity 97.5%;
Matches 474; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                             47 VROLLTEIFMKDPEOOEFMOAVREVAVSLOPVFEKRPELLPIFKOIVEPERVITFRVSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                     Indels
InterPro, IPR006096; GLFV_dehydrog_C.
InterPro, IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_I.
Pfam; PF02812; GLFV_dehydrog_I. 1.
PF10715; PR00082; GLFV_dehydrog_N: 1.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SEQUENCE 510 AA; 57343 MW; AC400045297AC64F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                       54.7%; Score 1375; DB 2;
60.0%; Pred. No. 6.7e-87;
ive 66; Mismatches 104;
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                                                                                                                                                                                                                                                                      Best Local Similarity 60.0%
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 TEKLLHYGAIPLSLSDSNGTIIEPNGFTAEQLKWYWDLKNIKR-GRLSEYTSMSSTAKYY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 GDRRKPWEL-DCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
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"Draft sequence of the Giardia lamblia genome.";
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
ransfer within and between prokaryotes and eukaryotes.";

BMC EVOL. Biol. 3:14-14(2003).

BMC EVOL. Biol. 3:14-14(2003).

BMS EVOL. Biol. 3:14-14(2003).

BMS COLOGARDER EVOL. Biol. 3:14-16(2003).

BMS COLOGARDER EVOL. BIOL.

COLOGARDER EVOL. BIOL.

BMS COLOGARDER EVOLUTION EV
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 446;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 39-33979-38030.
Glardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%; Score 1328; DB 2;
58.6%; Pred. No. 1e-83;
iive 65; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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                              CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.2%; Score 1361; DB 2; Length 1203; Best Local Similarity 59.3%; Pred. No. 1.9e-85; Matches 264; Conservative 65; Mismatches 108; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DBE1988BD4C21715 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                         GG; GO:0016491; F:oxidoreductase activity; IEA.
GG; GO:0006520; P:amino acid metabolism; IEA.
INTERPRO; IPRO06135; Exo-ando_phos.
INTERPRO; IPRO06095; GLFV dehydrog.
INTERPRO; IPRO06096; GLFV dehydrog.C.
INTERPRO; IPRO06096; GLFV dehydrog.N.
Pfam; PPO1312; Exo-ando_phos; I.
Pfam; PPO2028; GLFV dehydrog.I.
Pfam; PPO2012; GLFV dehydrog; I.
Pfam; PFO2012; GLFV dehydrog; I.
PROSITE; PSO0002; GLFPDHDRGNASE.
PROSITE; PSO0002; GLFPDHDRGNASE.
PROSITE; PSO00047; GLFV DEHYDROGENASE; I.
SEQUENCE 1203 AA; 139099 WW; DBE1988BD4C21715
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PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 AA
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                                                                                     preliminary data.
EMBL; AABL01000331; EAA20557.1; -.
HSSP; P24295; 1AUP.
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          Nature 419:512-519(2002).
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Eukaryota; Diplomonadi
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61

Gaps

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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 EFTGVLTGKNVKWGGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKOVTLSGSGNVAQFAC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGSDFDPKGKSDAEVWRFCQSFMTBLQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 EKLIQLGAKVLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 GDRRKPWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
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MEDLINE=92218410; PubMed=1559991;
Yee J., Dennis P.P.;
Yie J. Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene from the primitive eucaryote Giardia lamblia.";
J. Biol. Chem. 267:7539-7544(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.8%; Score 1327.5; DB 2; Length 449; Best Local Similarity 58.4%; Pred. No. 1.1e-83; Matches 261; Conservative 66; Mismatches 111; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                        100074; GLFV DEHYDROGENASE; 1.
449 AA; 49734 MW; 2397B34FBEBCAEE2 CRC64;
preliminary data.

EMBL; AACBO1000014; EAA41919.1; -.
HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:00016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; F:amino acid metabolism; IEA.
InterPro; IPR006099; GLFV dehydrog.
InterPro; IPR006099; GLFV dehydrog.
Pfam; PF00218; GLFV dehydrog.N:
Pfam; PR02812; GLFV dehydrog.N: I.
PRINTS; PR000082; GLFDHDRGNASE;
PROSITE; PR000074; GLFV DEHYDROGENASE; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 HPKNYQMGANIAGFLKVADSMIEQGCV
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIIYCPGKAANAGGVAVSGLEMTONRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 KGVMYGPAKASNAGGVSVSGLEMSQNSVRLQWTAEEVDQKLRGIMRGIFVACRDTAKKYG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
6 IEELIAVIKQRDGHMTEFRQAVEEVVDSLKVIFEREPKYIPIFERMLEPERVIIFRVFWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDRRKPWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 NYTGVLTPKGQEYGGSEIRPRATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKS---DTAVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 VROLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWL
                                                                                                                                                                                     -!- SUBUNIT: Homohexamer (By similarity).
-!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n
Similarity 58.2*; Pred. No. 1.8e-83;
60; Conservative 67; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 125 By similarity.
249 249 I -> L (in Ref. 2).
449 AA; 49766 MW; 5497B35209B549F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF022812; GLFV_dehydrog_N:
PF1NTS; PR00082; GLFV_dehydrog_N:
PR051TE; PS00074; GLFV_DEHYDROGENASE; I.
NADP; Oxidoreductase.
ACT_SITE
By SIMIlarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M84604; AAA29155.1; -. EMBL; U47632; AAB05400.1; -. PIR; A42489; A42489. HSSP; P24295; IAUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 260; Conservative
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123 GGKGGSDFDPKGKSDAEVWRFCQAFWTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 IRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 VGDRRKFWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=201755; PubMed=10710307; DOI=10.1126/science.287.5459.1809; MEDLINE=2017555; PubMed=10710307; DOI=10.1126/science.287.5459.1809; Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.8%; Score 1300.5; DB 2; Length 444; 57.4%; Pred. No. 8.2e-82; ive 72; Mismatches 104; Indels 15;
                                                                                                                                                                                                                                                                                                                 Glutamate dehydrogenase, NADP-specific.
OrderedLocusNames=NMB1710;
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48490 MW; 8B2CFCCA89EF7DAF CRC64;
                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00209; GLFV_dehydrog_N.
Pfam; PF00209; GLFV_dehydrog_N.
Pfam; PF02812; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
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Complete proteome.
SEQUENCE .444 AA; 48490 MW; 8B2CFCCA89
      422 NYVKGANIAGFVKVADAMLAQGVV 445
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:1809-1815(2000).
EMBL; AE002521; AAF42057.1;
PIR; H81050; H81050.
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Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseriaceae; Neisseria
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P24295; 1AUP.
TIGR; NMB1710; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 VROLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 GKGGSDFDPKGKSBAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CABLLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKONNSARISEYKSDTAVYVG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VDAFLERLKRRDPDOPEFHQAVEEVLRSLWPFLEANPHYLEAGIIERIVEPERAILFRVP 64
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
STRAIN=2043737; PubMed=10984043; DOI=10.1038/35023079;
MEDLINE=2043737; PubMed=10984043; DOI=10.1038/35023079;
Stover C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.B. W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 IIYCPGKAANAGGVAVSGLEMTONRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 DRRKPWELDCOVDIAFPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.1%; Score 1309; DB 2; Length 445; 59.2%; Pred. No. 2.1e-82; ive 55; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48856 MW; 643EB12BC84F3418 CRC64;
                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF028012; GLFV_dehydrog_N.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFV_DEHYDROMSE; 1.
      445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamate dehydrogenase.
Name=gdhA; OrderedLocusNames=PA4588;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004872; AAG07976:1; -.
                                                                                                                                                                                                                                                                                       Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 59.2°
Matches 263, Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; H83072; H83072.
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 445 AA;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
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Gaps

163

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(TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 449 AA;
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=160488;
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01-JUN-2003
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6
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302 YFEKQKPWGV--AAEIALPCATQNELDEBAAKTILLANGCYVVAEGANMPSTLGAVEQFIK 359
                                      AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 ITKNYTGVLTPKGQBYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                     360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMBL, ALIG2757; CABB5184.1; -.
REMBL, ALIG2757; LAUP.
REMBL, CO:0014354; F:glutamate dehydrogenase (NADP+) activity; IEA.
RGO; GO:0006520; P:amino acid metabolism; IEA.
RGO; GO:0006520; P:amino acid metabolism; IEA.
REMCFRO; IPR006095; GLFV dehydrog.
REMINETPRO; IPR006095; GLFV dehydrog.
REMBL, PR00208; GLFV dehydrog. N. 1.
REMM; PR00208; GLFV dehydrog. N. 1.
REMINS; PR00004; GLFV dehydrog. N. 1.
REMINS; PR00004; GLFV DEHYDROGENASE; 1.
RCOMLETE PR00014; GLFV DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                    GTRAIN=22491 / Serogroup A / Serotype 4A;

MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,

Klee S.R., Morelli G., Basham D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.

Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,

Majandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G., Erain of Neisseria

meningitidis 22411.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 444;
                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.5%; Score 1294.5; DB 2; Length Best Local Similarity 57.1%; Pred. No. 2.1e-81; Matches 256; Conservative 72; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48462 MW; DE7F1A7B8DD6F424 CRC64;
                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Glutamate dehydrogenase (EC 1.4.1.4).
Name=gdhA, OrderedLocusNames=NWA1964;
                                                                                                                                                                                     444 AA
                                                                                           462 ----NVDLAAGANIAGFTKVADAVKAQG 485
                                                                                                          416 KVGDTVNYVNGANIAGFVKVADAMLAQG 443
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 AA;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                       403
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104
284 YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 342
                                         243 YAAEKAIQLGAKVLTIVSDSNGFVLFPDSGMSEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
                                                                                                                                                                     AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 461
                                                                                                                                                                                                                                                                                                     105 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22423066; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Pouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hohelsel J., Straetz M., Heim S., Kiewitz C., Elsen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 VGDRRKFWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glutamate dehydrogenase.
Name-gdhA; OrderedLocusNames=PP0675;
Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. M.crobiol. 4.799-808 (2002). Embl. Actobiol. 4.799-808 (2002). HSSP; PA24295; JAUP. TIGR; PP0675; -.
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58.2%; Pred. No. 6.7e-81;
ive 55; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA; 48871 MW; EF1733B6ABC89627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF002012; GLFV_dehydrog_N; 1.
PRINTS; PR000087; GLFV_dehydrog_N; 1.
PRINTS; PR000087; GLFPURGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 AA
                                                                                                                                                                                                                                                                                                                                                                                                      485
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                                                                                                                                                                                                                                                                                                                                                                                                  ----NVDLAAGANIAGFTKVADAVKAQG
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REVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGP 128
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                                                                                                                                                                                                                                                                                       TGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYE 308
                                                                                                                                                                                                                                                                                                                  231 TGYGLVYFVLEVLKSLNIPVEKQTAVVSGSGNVALYCVQKLLHLNVKVLTLSDSNGYVYE 290
                                                                                                                                                                                                                                                                                                                                                                                    PNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVGDRRKPWELDCQVDIAFPCATQN 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLAAGANIAGFTKVADAVKA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 QNPQPSHWTRETVDEKLKEIMRNIFIACSENALKYTKNKYDLQAGANIAGFLKVAESYIE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W., Gardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Petres M., Allen J., Selengut J., Haft D., Mather M.W., Vaigholi S., Martin D.W., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Pavis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                    MTELORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEA
                             111 YKGGLRFHPSVNLSIVKFLGFEQIFKNSLTGLSMGGCKGGSDFDFKGKSDNEILKFCQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIDEHDABLLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMT
                                                                                                YKGGLRFHPSVNLSIMKFLAFEQIFXNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR06609; GLPV dehydrog.
InterPro; IPR06609; GLPV dehydrog. C.
InterPro; IPR00609; GLPV dehydrog_N.
Pfam; PF00208; GLFV dehydrog_N.
Pfam; PF0212; GLFV dehydrog; 1.
Pfam; PF00212; GLFV dehydrog N; 1.
PRINTE; PR00082; GLFDHPRGNASE; 1.
SEQUENCE 470 AA; S2546 MW; 50A37C23484C387A CRC64;
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Last annotation update)
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GO; GO:0006520; P.amino acid metabolism; IEA
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01-MAR-2003 (TrEMBLrel. 23, Last seque
01-OCT-2003 (TrEMBLrel. 25, Last annot
NADP-specific glutamate dehydrogenase.
ORFNames=PF14_0164;
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Nature 419:498-511(2002).
EMBL; AE014818; AAN36776.1; -
HSSP; P24295; IAUP.
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                           128 GKGGSDFDPKGKSDAEVMRFCQAFMSELYRHIGADCDVPAGDIGVGAREIGFMFGQYKRL
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                                                                                             225 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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HSSP; P24295; LAUP.
GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
Fam; PF00208; GLFV dehydrog.
Pfam; PF02812; GLFV dehydrog. 1.
Pfam; PF02812; GLFV dehydrog. 1.
PRINTS; PR0082; GLFPV dehydrog. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=GluDH; Synonyms=GDH;
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li L.H., Li M., Wu Y.S., Wang P.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12927; CAA73390.1; -.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
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Best Local Similarity
Matches 266; Conserv
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47 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 104
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PubMed-18209015 DOI=10.1186/1471-2148-3-14;
Andersen J.O., Roger A.J.;
Andersen J.O., Roger A.J.;
"Evolution of glutamate dehydrogenase genes: evidence for lateral gene
transfer within and between prokaryotes and eukaryotes.";
EMBL; AF533886; AAP83853.1;
HSSP; PA225; JAUP.
GO; GO:0016491; F:oxidoreductase activity, IEA.
GO; GO:0016491; F:oxidoreductase activity, IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
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Eukaryota, Parabasalidea, Trichomonada, Trichomonadida,
Trichomonadidae, Trichomonadinae, Trichomonas.
                                                                                                                                                                                                                                                                          445 AA; 48532 MW; B00DDE8E03A06D8A CRC64;
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Last annotation update)
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:anino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.C.
Pfam; PF00209; GLFV dehydrog.N.
Pfam; PF00209; GLFV dehydrog.N.
Pfam; PF00209; GLFV dehydrog.N.
Pfam; PF00209; GLFV dehydrog.N.
PF1TER: PR00812; GLFV dehydrog.N.
PROMITS; PR0082; GLFV DEHYDROGENASE; I.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                          Juery Match 51.1%; Score 1285; DB 2; Sest Local Similarity 58.4%; Pred. No. 9.8e-81; Aatches 261; Conservative 56; Mismatches 118;
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(TrEMBLrel. 25, L
(TrEMBLrel. 26, L
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                                                                                                          9 ISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDFEQQEFMQAV 68
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                        19;
     DB 2; Length 470;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown P.R.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
NADP-Glutamate dehydrogenase (EC 1.4.1.4).
Query Match 51.2%; Score 1286.5; DB 2; Best Local Similarity 55.2%; Pred. No. 8.3e-81; Matches 266; Conservative 64; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   London U.K
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Thesis (1994), University of London London U.K.
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Thasis (1994), University of London,
EMBL; Y18694; CAA77192.1; -.
EMBL; Y15166; CAA775437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Q923C4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGEVWRFCQSFMLELSRHIGGNTDVPAGDIGVGAREIGYMFGQYKRIKNVFEGVLTGKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 QEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLSDSQGYVYEPNGFTREQLOAVQDMKK--KNNSARISEYKSDTAVY-VGDRRKPWELD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 CQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAGGVAVSGLEMTONRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAG 473
                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GPRVQFNSAIGPYKGGCRFRGNVNLSILKFLGFEQVFKNSLTTLPMGGGKGGSDFDPAGK
                                                                                                                                                                                                                                                                                                                                                                 4 RDPDQKEFIQAVTEVLTSLVPILEKEPKYQKLLPALVEPERVIMFRVPWVNDKGEMMVNR
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                 DB 2; Length 437;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 51.1%; Score 1284.5; DB 2; Length Local Similarity 59.0%; Pred. No. 1e-80; e8 255; Conservative 56; Mismatches 118; Indels
                                                                                                                                                                                                  437 AA; 47861 MW; 75205554DAFBEF96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
InterPro; IPR006095; GLFV dehydrog.
R InterPro; IPR006095; GLFV dehydrog_C.
R InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
R Pfam; PF02812; GLFV_dehydrog_N.
R PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
NON_TER
SEQUENCE 437 AB.
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FKRVADAMLAYG 435
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Best Local Si
Matches 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 WGVPC--TLAFPCATQNEINLEDAKLLRKNGCILVGEGANMPSTVDAINLFKSNNIIYCP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 GKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 SKAANAGGVAISGLEMSQNFQFSHWTRETVDEKLKEIMRNIFIACSENALKYTKNKYDLQ 421
                                                                                                                                                                                        65
                                                                                                                                             DPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGV
                                                                                                                                                                                                                                                                                                                                                                                                              LTPKGQEYGGSBIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCP
                                                                                                                                                                                                                                   112 LQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDF
                                                                                                       Gaps
                                                          Ouery Match 50.3%; Score 1265; DB 2; Length 442; Best Local Similarity 58.8%; Pred. No. 2.4e-79; Matches 258; Conservative 57; Mismatches 114; Indels 10;
PROSITE; PSO0074; GLFV DEHYDROGENASE; 1.
SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCE4CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8, 2005, 02:43:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 AGANIAGFTKVADAVKAQG 485
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Job time: 90.1553 secs
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                                                               Query Match
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 8, 2005, 02:27:13; Search time 21.1308 Seconds (without alignments) 2217.496 Million cell updates/sec Run on:

US-10-627-886-24 2513 1 MAVSLEEQISAMDATTGDFT......GANIAGFTKVADAVKAQGAV 487 Title: Perfect score: Sequence:

Scoring table:

. 283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | | | | | | | | deh | fic | fic | dehy | deh

 | | NADP-specific glut | NADP-specific glut
 | fic | deh | glutamate dehydrog | NADP-specific glut | fic | | | glutamate dehydrog |
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| QI | \$17949 | A42489 | H83072 | H81050 | B81825 | A64053 | T10487 | D98019 | H95151 | E83912 | E75362 | DEECEN

 | F96990 | C90937 | G85785
 | A11503 | S32227 | A33504 | AF0710 | AI1144 | AE0483 | D64567 | S22403 | B95277
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 | 44 | 45 | | 4. |
| Query
Match | 97.3 | 52.7 | 52.1 | 51.8 | 51.5 | 49.3 | 48.3 | 48.3 | 48.2 | 48.2 | 48.0 | 47.8

 | 47.7 | 47.7 | 47.7
 | 47.3 | 47.2 | 47.0 | 47.0 | 47.0 | 45.9 | 45.8 | 45.5 | 45.5
 | 45.3
 | 45.1 | 44.6 | 44.4 | 44.1 |
| Score | 2446 | 1324.5 | 1309 | 1300.5 | 1294.5 | 1238 | 1214.5 | 1214 | 1212 | 1210.5 | 1205.5 | 1201

 | 1199 | 1198 | 1198
 | 1189.5 | 1185 | 1182 | 1181 | 1180.5 | 1153 | 1150 | 1143 | 1142.5
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 | 1133.5 | 1121.5 | 1115.5 | 1109 |
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444 2 1104.87 91utamate deh 1214.5 48.2 448 2 1098019 NADP-specific 1212.6 48.2 448 2 149551 NADP-specific 1205.5 48.2 447 1 DEECEN 91utamate deh 1199.6 47.7 443 2 P56590 NADP-specific 1198.7 47.7 447 2 G85785 NADP-specific 1189.5 47.7 447 2 A50483 91utamate deh 1189.5 47.0</td> <td>Query Query 2446 97.3 523 1 \$17949 glutamate deh 1324.5 52.7 449 1 A42489 glutamate deh 1309 52.1 445 2 H83072 glutamate deh 1309.5 51.5 444 2 B8125 glutamate deh 1234.5 51.5 444 2 B8125 glutamate deh 1234.5 51.5 444 2 B8125 glutamate deh 1214.5 48.2 448 2 B8125 glutamate deh 1214.5 48.2 448 2 B8125 glutamate deh 1210.5 48.2 45212 NADP-specific glutamate deh 1205.5 48.0 424 2 E83912 glutamate deh 1199 47.7 447 2 C9037 NADP-specific 1198 47.7 447 2 A1103 glutamate deh 1189.5 47.7 447</td> <td>Query Query 2446 97.3 523 1 817449 91utamate deh 1324.5 52.7 449 1 A42489 91utamate deh 1300.5 51.9 444 2 H83072 91utamate deh 1300.5 51.6 444 2 B81825 91utamate deh 1214.5 51.5 444 2 D8019 91utamate deh 1214.5 48.2 2 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deh 1234.5 51.5 444 2 B8125 glutamate deh 1234.5 51.5 444 2 B8125 glutamate deh 1214.5 48.2 448 2 B8125 glutamate deh 1214.5 48.2 448 2 B8125 glutamate deh 1210.5 48.2 45212 NADP-specific glutamate deh 1205.5 48.0 424 2 E83912 glutamate deh 1199 47.7 447 2 C9037 NADP-specific 1198 47.7 447 2 A1103 glutamate deh 1189.5 47.7 447 | Query Query 2446 97.3 523 1 817449 91utamate deh 1324.5 52.7 449 1 A42489 91utamate deh 1300.5 51.9 444 2 H83072 91utamate deh 1300.5 51.6 444 2 B81825 91utamate deh 1214.5 51.5 444 2 D8019 91utamate deh 1214.5 48.2 2 D98019 91utamate deh 1214.6 48.2 2 B81825 91utamate deh 1210.6 48.2 48.9 2 R8281 121.6 48.2 2 B81825 91utamate deh 1205.5 48.0 424 2 E83312 NADP-specific 1205.5 48.0 424 2 E83562 91utamate deh 1198 47.7 447 2 C9037 NADP-specific 1189.7 447 2 C9037 NADP-specific 11 | Query Query 2446 97.3 52.1 449 1 A42489 Glutamate deh glutamate d |

probable glutamate	glutamate dehydrog	glutamate dehydrog	glutamate dehydrog	hypothetical prote	glutamate dehydrog	NAD-specific gluta	glutamate dehydrog								
T41492	S17907	A25275	851960	B96556	T45284	G72305	F83852	A70055	G69933	G89862	G84220	D75176	F83989	F84142	B81079
~	~	Н	~	~	~	~	7	~	7	~	~	~	~	~	N
451	459	454	457	624	416	416	421	424	426	414	372	420	430	420	421
43.5	42.5	41.3	40.7	39.7	23.1	22.9	22.0	21.9	21.7	21.7	21.3	21.1	21.1	21.0	21.0
1092	1067.5	1037.5	1022	997.5	579.5	576.5	552.5	551	545.5	544.5	536	530	529.5	527.5	527.5

ALIGNMENTS

RESULT 1	
S1/343 glutamate dehydrog(N,Alternate names: C.Snecies Chlorel	S17337 glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment) Ablternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase C.Species: Chlorella expekintana
 C; Date: 30-C	C. Deceis 30-Jun-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004 C. Accession: 817940- 817950- 819030
R; Cock, J.M.	Strocks.com; Living S. Living B. S. S. Schmidt, R.R. S. Plant M. Biol. 17. 102-104. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911. 1911.
 A; Title: A nuclear g A; Reference number:	A:Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADF A;Reference number: S17949; MUID:92032762; PMID:1718478
 A, Accession: S17949 A, Molecule type: DNA	S17949 ype: DNA
 A;Residues:	A;Residues: 1-523 <coc></coc>
A; Accession: S17950	S17950
A;Molecule type: mRNA A:Residues: 1-523 <co< th=""><th>A;Molecule type: mRNA A:Remidnem: 1-523 <coc2></coc2></th></co<>	A;Molecule type: mRNA A:Remidnem: 1-523 <coc2></coc2>
 A; Cross-refe	A;Cross-references: EMBL:X58832; NID:g18272; PIDN:CAA41636.1; PID:g18273
 R;Schmidt, R.R.	R;Schmidt, R.R. submitted to the RWR. Data Library April 1991
A, Reference	A;Reference number: S19030
 A, Accession: S19030	S19030
 A;Molecule t	AfMOLECULE TYPE: DNA
A; Cross-refe	
C, Genetics:	
A;Genome: nuclear A:Introns: 6/2: 2	Ajiebnome: mudicaar Aiintromas: 6/2: 29/1: 40/3: 56/3: 85/3: 127/3: 149/3: 175/1: 163/3: 211/1: 246/1: 272/2
C;Superfamil	(NAD(P)+)
F;202/Bindir	F;202/Binding site: substrate (Lys) #status predicted
 Query Matc Best Local	97.3%; Score 2446; DB 1; Length 523; ilarity 97.5%; Pred. No. 1.5e-173;
 Matches 4	m
 ò	2 AVSLEBQISAMDATTGDFTALQKAVKQMATKAGTBGLVHGIKNPDVRQLLTEIFMKDPEQ 61
 Db 3	38 AKRIRSKSPRMDATTGDFTALQKAVKQMATXAGTEGLVHGIKNPELRQLITEIFMKDPEQ 97
 0,7	62 QEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ 121
 g qq	98 QEFMQAVREVAVSLQPVFEKRPELLIPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ 157
Qy 122	2 YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGKGGSBFDPKGKSDAEV 181
Db 158	
Qy 182	2 MRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG 241
 Db 218	

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Glucamate dehydrogenase PA4588 [imported] - Reeudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Diaces (15.56p-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83072
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Teference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83072
A;Status: preliminary
A;Residues: 1-445 cSTO>
A;Cross-references: UNIPROT:Q9HVJ7, GB:AE004872; GB:AE004091; NID:g9950829; PIDM:AAG07977
C;Genetics:
A;Gene: gdha, PA4588
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
#81050
glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (stra glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Cbate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81050 R;C; H81050 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AARKVMEMGGKVISLSDSECTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 GKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.1%; Score 1309; DB 2; 159.2%; Pred. No. 2.6e-89; ive 55; Mismatches 120;
  487
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                        423 HPKNYQMGANIAGFLKVADSMIEQGCV
--VDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 59.24
Matches 263; Conservative
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A42489
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
NyAlternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C;Species: Glardia lamblia
C;Accession: A42489
R;Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A;Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A;Reference number: A42489; MUID:92218410; PMID:155991
A;Rocession: A42489
A;Molecule type: DNA
A;Residues: 1-449 < YYEB-
A;Cross-references: UNIPROT:P28724; GB:M84604; NID:g159108; PIDN:AAA29155.1; PID:g159109
A;Note: sequence extracted from NCBI backbone (NCBIN:94071, NCBIP:94074)
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase
F;125/Binding site: substrate (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGSDFDPKGKSDAEVMRFCQSFMTBLQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGSDFDPKGKSDNEVMRFCQSFWTELQRHVGADTDVPAGDIGVGAREIGYLYGQYKRLRN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKS---DTAVYV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:: || ||: ||| | : : : || |:| : : | : || |:| EKLIQLGAKVLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDRRKFWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G--KKPWECFEGOMDCIMPCATONEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA 362
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                      278 SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                                                                                            338 SQGYVYEPNGFTREQLQAVQDMKKKONSARISEYKSDTAVYVGDRRKFWELDCQVDIAFP
                                                                                                                                                                                                  CATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                                                                                                   GLEMTQNRMSLNWTREEVRDXLERIMKDIYDSAMGPSREYNVDLAAGANIAGFTKVADAV
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                                                                                                                                                                         CATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
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                                                                                                                                                                                                                                                                                                                                                   KAQGAV 487
                                                                                                                                                                                                                                                                                                                                                                                           KAQGAV 523
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463 421

15;

Length 444;

46 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV

123 GGKGGSDFDFKGKSDABVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK 182 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 283

GGKGGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR

242

224

164

----NVDLAAGANIAGFTKVADAVKAQG 485 |: ||||||| |||||| KVGDTVNYVNGANIAGFVKVADAMLAQG 443

462

AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 461

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Query Match
Best Local Similarity 57.1%
Matches 256; Conservative
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ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Carandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8. A; Reference number: A81000; MUD:20175755; PMID:10710307
A; Residues: 1-444 < TET-
A; Cross-references: UNIPROT:091771; GB:AE002521; GB:AE002098; NID:G7226962; PIDN:AAF4205
A; Experimental source: serogroup B, strain MC58
C; Genetics: NMB1710
C; Superfamily: glutamate dehydrogenase (NAD(P)+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 YFEKQKPWGV--AABIALPCATQNELDEBAAKTILANGCYVVAEGANMPSTLGAVEQFIK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 VGDRRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402
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                                                                                                                                                                                                                               444;
                                                                                                                                                                                                                              Length
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Glutamate dehydrogenase (NADP) (EC 1.4.1.4) NMA1964 [imported] - Neisseria meningitidis CiSpecies: Neisseria: Neisser
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A,Gene: gdhA, NWA1964 C,Superfamily: glutamate dehydrogenase (NAD(P)+) C,Keywords: oxidoreductase

Genetics:

SDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNY 228 109 AGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFXNSLTTLPMGGGKGG 51 LTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRVSWLDD 16; Length 449; Indels Query Match
49.3%; Score 1238; DB 2;
Best Local Similarity 55.6%; Pred. No. 5e-84;
Matches 247; Conservative 64; Mismatches 117; 11 169 ሯ 셤 Š 셤 ò

168

70

Gaps

A;Residues: 1-449 <TIGR>
A;Cross-references: UNIPROT:P43793; GB:U32704; GB:L42023; NID:g1573143; PIDN:AAC21858.1, C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase

A;Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

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                                                                                                                                                                                                                                                                                                                                              Glucamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola C; Species: Prevotella ruminicola C; Species: Prevotella ruminicola C; Species: Prevotella ruminicola C; Date: 16-Jul-1999 #text_change 09-Jul-2004 C; Accession: 110487 M.

R; Wen, Z.T.; Morrison, M.

submitted to the EMBL Data Library, December 1996
A; Accession: 110497
A; Accession: 110497
A; Accession: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-44 < VMEN.
A; Residues: 1-44 < VMEN.
A; Cross-references: UNIPROT: P95544; EMBL: U82240; NID: g1772845
A; Experimental source: strain B14
C; Superimental source: strain B14
C; Superfamily: glutamate dehydrogenase (NAD(P)+)
C; Keywords: NADP; oxidoreductase
                                                                                                                                                                                                461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 ARPW--GEKADIATPCATQDEINEAEAKTLIANGVFAVSEGANMPTEPAAIKVFQDAKIL 361
                                             LLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRK 348
                                                                                                251 ALSLGAKVVTCSDSSGYVYDPNGFTTEKLAALFDI-KNTKRGRVKDYAEQFGLQYFEGKR 309
                                                                                                                                         PWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYC 408
                                                                                                                                                         49 QLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVSWL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 RKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGII 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM--GPSRRYNVD 464
SDFDPKGKSDAEVMRFCQALMAELYRHVGADTDVPAGDIGVGGREVGYLAGYMKKLSNQS 190
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                                                                                                                                                                                                                                                    310
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    Streptococcus pneumoniae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 IQSVFETVKARNGHEAEFLQAVEEFFNTLEPVFEKHPEYIEBNILARITEPERVISFRVP
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362 YCPGKASNAGGVATSGLEMSQNSERLSWTREEVDTKLHNIMDEIHANCVKYGTEPDGYIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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8
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// Score 1214; DB 2; Length 4
// Pred. No. 3e-82;
62; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: gdhA
C,Superfamily: glutamate dehydrogenase (NAD(P)+)
C,Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 -DLAAGANIAGFTKVADAVKAQGAV 487
                                                                        442
                                                         |||:||| ||| ||: |||
422 YVKGANVAGFMKVAKAMMAQG
                                    LAAGANIAGFTKVADAVKAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.7%;
Matches 248; Conservative 6;
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91 63

Gaps

17;

Indels

48.2%; Score 1210.5; DB 2; dlarity 54.7%; Pred. No. 5.6e-82; Conservative 71; Mismatches 121;

Similarity

Query Match Best Local Simil Matches 252; (

Length 458;

211

64 IVEPERVISFRVPWVDDQGNVQVNRGFRVQFNSALGPYKGGLRFHPSVNASIIKFLGFEQ 123

IVEPERVITERVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQ

92

38 LVHGIKNPDVROLLTEIF----MKDPEQOEFMQAVREVAVSLOPVFEKRPELL--PIFKQ

REIGYLFGQYKRITKNY-TGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKG 270

152 IFKNSLITLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGA

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on, Journal H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A-Authors: Loffuel, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Reference number: A5000; MUID:21357209; PMID:11463916
A; Reference number: A5000; MUID:21357209; PMID:11463916
A; Residue type: DNA
A; Residue: preliminary
A; Residue: 1-448 exunc.
A; Residues: 1-440 exunc.
A; Residues: 1-450 exunc.
A; Residues: 1-450 exunc.
B; Residue type: DNA
A; Residue t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNV- 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S IQSVFETVKARNGHEAEFLQAVEEFFNTLEPVFEKHPEYIEENILARITEPERVVSFRVP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLDDAGNIQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 NQPDAGVLTGKPLGFGGSLIRPEATGYGLVYYTEEMLKANGNSFAGKKVVISGSGNVAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 IFYGPAKAANAGGVAVSALEMSQNSLRLSWTREEVDGRLKDIMTNI FNTAKTTSETYGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 DRRKPWELDCOVDIAFPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.2%; Score 1212; DB 2; Best Local Similarity 55.5%; Pred. No. 4.2e-82; Matches 247; Conservative 63; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Genetics;
;Gene: SP1306
;Superfamily: glutamate dehydrogenase (NAD(P)+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 -DLAAGANIAGFTKVADAVKAQGAV 487
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KRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSA 330

271

244

300

331

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449 418

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389

212 184 STVVVSGSGNVSIYAMEKAMQLGAKVVACSDSGGYVYDKNGIDLQTVKRLKEVERK-

243

388 357

RISEYKSD - - TAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGA NMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMK 448

487 458

DIYDSAMGPSRRYNV--DLAAGANIAGFTKVADAVKAQGAV

> NADP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C-12 GB:BA000004; NID:910174613; PIDN:BAB058 and F.; Hir Nor-specials: Bacillus halodurans (Specials Bacillus halodurans) | Bacillus halodurans (Specials Bacillus halodurans) | Bacillus halodurans | C;Specials Bacillus halodurans | C;Specials Bacillus halodurans | C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 | C;Accession: B83912 | B;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Acids Res. 28, 4317-4331, 2000 | A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Accession: B83912 | A;Access

;Gene: gdhA ;Superfamily: glutamate dehydrogenase (NAD(P)+)

Glutamate dehydrogenase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 0.3 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75362
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.; Sinth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75362
A;Accession: E75362
A;Accession: E75362
A;Accession: E7544 < WHI>
A;Residues: 1-424 < WHI>
A;Crose-references: UNIPROT:Q9RTN9; GB:AE002013; GB:AE000513; NID:g6459484; PIDN:AAF1127
A;Crose-references: Strain R1
C;Genetics: 4 122 SSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVM 182 9 65 MOAVREVAVSLOPVFEKRPELL--PIFKQIVEPERVITFRVSWLDDAGNLOVNRGFRVQY Gaps 7; Length 424; Indels = DB 2; 48.0%; Score 1205.5; DB 2; 56.2%; Pred. No. 1.2e-81; tive 61; Mismatches 119; A, Map position: 1 C; Superfamily: glutamate dehydrogenase (NAD(P)+) Best Local Similarity 56.21 Matches 240; Conservative A, Gene: DR1718 123 61 Query Match Best Local S ઠે 셤 à g

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MADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum C; Species: Clostridium C; Species: Clostridi
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GGenetics:
A;Genetics: CAC0737
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
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                                                                                                                                                                                                                        127 GKGGSDPDFKGKSEGEVWRFCQALMTELYRHLGADTDVPAGDIGVGGREVGFWAGMMKKL
                                                                                                                                                                                                                                                                                                                                                                 SINTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMGFEGMRVSVSGSGNVAQY
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                                                                                                                                                                                  GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
                                                                                                                                                                                                                                                                                                                     225 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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                                        WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFRQIFKNSLTTLPMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRRKFWELDCQVDI AFPCATQNEI DEHDAELLI KHGCQYVVEGANMPSTNEA I HKYNKAG
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47.7%; Score 1199; DB 2;
Best Local Similarity 54.4%; Pred. No. 3.8e-81;
Matches 242; Conservative 69; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                        241 GGTVVDEDGFTYDKLAVLMDIKNERR-GRVEDYAREVGABFRPGVRPW--DVPVDVALPC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 LEMSQNAORLSWTREEVDORLKSIMSAIHDSCLEYGRRPDRHVSYLDGANIAGFVKVATA 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                            181 LLRPEATGYGTVYFVEHMLRDQRMEMEGLRVSVSGSGNVAQYAIEKALHLGAHVLTASNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRR--YNVDLAAGANIAGFTKVADA
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                                                                                                                                         243 BIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                             ATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSG
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C;Superfamily: glutamatte dehydrogenase (NAD(P)+)
C;Keywords: homohaxamer; NADP; oxidoreductase
F;128/Binding site: substrate (Lys) #status predicted
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Best Local Similarity 54.0%
Matches 241, Conservative
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MREQGVL 424
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Cyaccession: G85785

K; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: G85785

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-447 < 4570>

A; Cross-references: UNIPROT: Q8XDW9; GB: ABC005174; NID: G12515786; PIDN: AAG56747.1; GSPDB:CAPERITE CONTROL STREET 
                                                        - Escherichia coli (strain 0157:H7, sul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                            GB5785
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (straın C;Species: Bscherichia coli (c;Species: Bscherichia coli (c;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: glutamate dehydrogenase (NAD(P)+)
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A;Gene: gdhA
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
C90937
NADP-sepecific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub
C;Species Escharichia coli #cevision 18-Jul-2001 #text_change 09-Jul-2004
C;Species 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90937
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <AAAY
A;Coss-references: UNIPROT:Q8XDW9; GB:BA000007; PIDN:BAB35890.1; PID:g13361934; GSPDB:G
C;Genetics:
A;Gene: EC82467
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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                                                                                                                                                       403 AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 462
                                                                                                                                                                                         404
                                                                               TEGCDGIWKLKC--DIALPCATQNEIDENSAKTLIANGCYAVGEGANMPSTIEAVDLFIK 357
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244 ANQKATQLGAKVVAMSDSNGYIYDANGINLNTIRKIKEVERK----RIHEYTKYHPNASY 299
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GenCore version 5.1.6
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1 MAVSLEEQISAMDATTGDFT......GANIAGFTKVADAVKAQGAV 487 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp20028; *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aau98954 Mature NA	Adq36729 Mature NA	Aaw15408 NADP-spec	Aau98951 NADP-glut	Add36709 NADP-spec		Aau98950 NADP-glut	Adq36707 NADP-spec		Aaw15412 NADP-spec	Aau98955 Mature NA	Adq36731 Mature NA	Abu38763 Protein e	Abo71900 Pseudomon	Adp08330 Neisseria		Pro	Aau72986 Neisseria	Abu38117 Protein e	Abu39614 Protein e	Ads24914 Bacterial	Adn27186 Bacterial	Abul7276 Protein e	Ada34438 Acinetoba	Abp65630 Bifidobac
ID	AAU98954	ADQ36729	AAW15408	AAU98951	ADQ36709	AAW15407	AAU98950	ADQ36707	AAW15411	AAW15412	AAU98955	ADQ36731	ABU38763	ABO71900	ADP08330	ABP77942	ABU37205	AAU72986	ABU38117	ABU39614	ADS24914	ADN27186	ABU17276	ADA34438	ABP65630
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448 6 ABU29386 448 8 AAH9147 449 5 AAB88536 449 6 ABU30172 449 6 ABU30172 449 6 ABU30172 449 6 ABU49018946 449 6 ABU49140 448 6 ABU46100 448 8 ADX28251 448 6 ABU46100 448 8 ADX28251 448 6 ABU20518 444 6 ABU20518 447 2 AAW608092 447 2 AAW608092	Abu29386 Protein e	Adh97147 E. faecal	Aau91467 Haemophil	Aab88536 Haemophil	Abu30172 Protein e	Abp28423 Streptoco	Adh85999 Enterococ	Abu44405 Protein e	Abu38946 Protein e	Adk47974 Streptoco	Abu46100 Protein e	Abu01740 S. pneumo	Adh97149 E. faecal	Ads28251 Bacterial	Abu23354 Protein e	Adn17964 Bacterial	Abu20518 Protein e	Aaw08092 Glutamina	Aaw60830 E. coli g	Abul5360 Protein e
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	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

NADP-specific glutamate dehydrogenase, NADP-GDH; alpha subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme. Mature NADP-glutamate dehydrogenase alpha subunit. AAU98954 standard; protein; 487 AA (first entry) 24-SEP-2002 AAU98954; AAU98954

Chlorella sorokiniana. US2002062495-A1.

23-MAY-2002.

98US-00070844. 01-MAY-1998; 98US-00070844. 01-MAY-1998;

(SCHM/) SCHMIDT R R. (MILL/) MILLER P.

<u>ь</u> Schmidt RR, Miller

WPI; 2002-499691/53. N-PSDB; ABK51025.

Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress

Claim 7; Page 27-28; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammoniatoricity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in

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                                                                                 MAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPE
                                                                                                                     QGEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRV
                                                                                                                                                            QYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAE
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                                                                      1 MAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPE
                                                                                                           QQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRV
                                                                                                                                               QYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGCKGGSDFDPKGKSDAE
                                                                                                                                                                                                                     GSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLS
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Pred. No. 5.6e-231;
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the method of the invention
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Matches 487; Conservative
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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH ADD36707, ADD36729, a beta subunit of NADP-specific GDH ADD36711), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADD36710 or ADD36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmotic stress, and composition of the crop or plant. The present
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Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGKGGSDFDPKGKSDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQBYG
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                                                                                                                                                                  Claim 7; SEQ ID NO 24; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      method of the invention.
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chloralia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                                                                                    GLEMTQNRMSLAWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV 506
                                                                                                                        CATONE IDEHDAELLIKHGCOYVVGGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                              GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                      SQGYVYEPNGFTREQLQAVQDMXKKONSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
                                             SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRKKPWELDCQVDIAFP
                                                                                                 CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
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100.0%; Pred. No. 1.8e-230;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADP-glutamate dehydrogenase beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAU98951 standard; protein; 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHM/) SCHMIDT R R.
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Best Local Simil
Matches 486; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase inducible, chlorolas sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding NADF-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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                                                                                                                                        Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
                                                                                                 NADP-specific glutamate dehydrogenase beta-subunit precursor.
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                                                                                                                                                                                                  Chlorella sorokiniana; strain UTEX 1230,
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                                                                                                                                                             chloroplast; transgenic plant.
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N-PSDB; AAT64530, AAT64543.
                                       (revised)
(first entry)
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                                     17-OCT-2003
10-JUL-1997
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AAW15408
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                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                     87 QEFWQAVREVAVSLQPVFBKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ
                                                                                          MRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
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                  AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
                                            QEFMQAVREVAVSLQPVFEXRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ
                                                                              YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                 MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                      SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
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                                                                                                                                                                                                                                                                                                                                                                    ADQ36709 standard, protein, 512 AA
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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polynocleotide encoding a polypeptide having glutamate debytosgenase oplynocleotide encoding a polypeptide is an alpha subunit of NaDP-specific GDH (ADQ36719), a beta subunit of NaDP-specific GDH (ADQ36719), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, sequence is the precursor protein of the crop or plant. The present sequence is the precursor protein of the beta subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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7; SEQ ID NO 4; 36pp; English.
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10-JUL-1997
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sockiniana NADP-glutamate dehydrogenase alpha subunit, used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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100.0%; Pred. No. 1.9e-230;
ive 0; Mismatches 0;
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N-PSDB; ABK51007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokimiana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT6459-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
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                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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                   NADP-GDH; alga; nitrogen metabolism;
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Pred. No. 1.9e-230;
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Best Local Similarity 100.0%; Pred. No. 1.9
Matches 486; Conservative 0; Mismatches
                                                                          Chlorella sorokiniana; strain UTEX 1230
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                                      plant
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                                      transgenic
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                                      chloroplast;
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Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmocic stress, by transforming plant cell with nucleic acid having glucamate dehydrogenase activity.
                                                                                                                  281 SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                      161 YSSAIGPYKGGLRPHPSVNLSIMKPLAFEQIFKONSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                                                         341 SQGYVYEPNGFTREQLQAVQDMKKKONNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFP
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                                                                  MRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                    MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                        SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
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                                                                                                                                                                                   CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                                                                                                                                                                                                       NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.
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                                                                                                                                                                                                                                                                                                                                ADQ36707 standard; protein; 526
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N-PSDB; ADQ36706.
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(GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADG367107, ADG36729), a beta subunit of NADP-specific GDH (ADG36719), or their fragments, which exhibits GDH activity. The polymucleotide is operably liked to a polymucleotide encoding a chloroplast transit peptide comprising ADG36710 or ADG36711, or their fragments that exhibit chloroplast transit activity. The method is useful fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polymucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, semplies as and composition of the crop or plant. The present sequence is the precursor protein of the alpha subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 1.9e-230; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.8%; Score 2508; DB 8;
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                                                                                                                                                                                                                                                                                                                                       2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.

They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (CFPET, increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.

(Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQBYG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                        DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKAPDVRQLLTEIFMKDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VMRFCQSFMTELORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 DSQGYVYEPNGFTREQLQAVQDMKKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSQGYVYEPNGFTREQLQAVQDMKKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCATQNEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.7%; Score 2505; DB 2; Length 487; 99.8%; Pred. No. 3.3e-230; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                              Claim 1; Page 44-46; 61pp; English
                                                                                95US-00541033
                                             96WO-US015921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.8
Matches 486; Conservative
                                                                                                                                                   Miller P;
                                                                                                                (UYFL ) UNIV FLORIDA
                                                                                                                                                                                    WPI; 1997-226226/20.
N-PSDB; AAT64547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 487 AA;
                                           03-OCT-1996;
                                                                                06-OCT-1995;
                                                                                                                                                                                                                                                                             plant cells.
                                                                                                                                                     Schmidt RR,
            10-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana. They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (bref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or bete subunits or precursor and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 AVSLOPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLOVNRGFRVQYSSAIGPYKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.1%; Score 2465; DB 2; Length 476; 100.0%; Pred. No. 2.1e-226; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                NADP-specific glutamate dehydrogenase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlorella sorokiniana; strain UTEX 1230,
                                                                                                                                                                                                           AAW15412 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 48-50; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chloroplast; transgenic plant
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(first entry)
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   487
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                                                      481 VKAQGAV
481 VKAQGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT64548
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10-JUL-1997
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                                                                                                                                                                                                                                                                           AAW15412;
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Nitrogen metabolism; plant, glutamate dehydrogenase; GDH; enzyme;
beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
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                                                                                                                                                                                                             GLRFHPSVNLSIMKFLAFBQIFKNSLTTLFMGGGKGGSDFDFKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                                                                                 121 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFCQSFWTE
                                                                                                                                                                                                                                                                                                                                                                                          PTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                       12 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                                                                                                          1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                                                                                                                                    LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 476;
                                                                                                 Indele
                                                              Score 2465; DB 5; L
Pred. No. 2.1e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mature NADP-specific GDH beta subunit, SEQ ID 26.
                                                98.1%; Sc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ36731 standard; protein; 476
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                                                                                              Matches 476; Conservative
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N-PSDB; ADQ36730.
                                                                              Similarity
                           Sequence 476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved cemotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the method of the invention
                                                                                                                                                                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                       311
                                                                                                                                                                                                                                 431
241 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
                                                                                                                                   GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                           181 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGGEYGGSEIRPEATGY
                                                                                                                                                                                                               FTREOLOAVODMKKKNNSARISEYKSDTAVYVGDRRKPWBLDCOVDIAPPCATONEIDEH
                                                                                                                                                                                                                                                                                        DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 487
                                                                                                                                                                                                                                                                                                                                                                                    NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature NADP-glutamate dehydrogenase beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU98955 standard; protein; 476
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N-PSDB; ABK51026.
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WO200277183-A2 03-OCT-2002

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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polymeptide having glutamate dehydrogenase (GDH) activity. The polymeptide having glutamate dehydrogenase (GDH) activity. The polymeptide is an alpha subunit of NADP-specific GDH AD036739, a beta subunit of NADP-specific GDH (AD036731) to their fragments, which exhibits GDH activity. The polymucleotide is operably linked to a polymucleotide encoding a chloroplast transit peptide compartising AD036710 or AD036711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polymucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to amomia toxicity, osmotic stress, and composition of the crop or plant. The present sequence is the mature beta subunit of the NADP-specific GDH used in the
osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                                                  Claim 7; SEQ ID NO 26; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method of the invention
##X8X5666666666668X8X8X8
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Sequence 476 AA;

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                                                                                                                                                                                                      420
                                                                                                                         72 AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 131
                                                                                                                                                                                    GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFCQSFWTE 191
                                                                                                                                                                                                                                                                                                            GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 311
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                                                                              12 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                 LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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 98.1%; Score 2465; DB 8; Length 476;
                                Indels
                100.0%; Pred. No. 2.1e-226; ive 0; Mismatches 0;
              Best Local Similarity 100.
Matches 476; Conservative
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Query Match
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                              Protein encoded by Prokaryotic essential gene #24290.
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                      ABU38763 standard; protein; 445
                                                                     (first entry)
                                                                                                                                             Pseudomonas aeruginosa
                                                                       19-JUN-2003
                                               ABU38763;
RESULT 13
             ABU38763
                       SXXXXXXXXXXX
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the fell antisense sequences given in the specification where expression of the fell antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway compliferation or the activity of a gene in an operon required for cut proliferation or that inhibits cellular proliferation of the gene product or that has an activity against a biological pathway in which a proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, 8 activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (12) determining the extent to to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound, 8 activity; (11) a culture comprising strains in which ach of the strains is present in a culture or collection of strains; or proliferation of an organism. The antisense uncleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. the target profice sesential genes uncleic acids are useful for dang discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. the target provery programs.

C. the target proverspread for the present sequence is encoded by one of the target proversion sector. The present s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                        Haselbeck R. Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 66687; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                        Malone C,
Carr GJ,
                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-029926/02.
N-PSDB; ACA42633.
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                                                                                                                                                                                                                                                                                                                                        Wang |
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47 VROLLTEIFMKDPEQOEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 104 Gaps 9 Length 445; 52.1%; Score 1309; DB 6; Length 44 59.2%; Pred. No. 7.7e-116; ive 55; Mismatches 120; Indels Matches 263; Conservative Similarity ß Query Match Local ઠે g 105 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 164

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15-NOV-2002; 2002GB-00026734.
27-MAR-2003; 2003GB-00007131.
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                                                                                Query Match
Best Local Similarity 59.2°
Matches 263; Conservative
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                                                                                                                                                                                       463
                                                                                                        245 AARKVMEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL 303
                                                                                                                                          404
               125 GKGGSDPDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL 184
                                                                                            CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 344
                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment copathological conditions resulting from bacterial infection.
                                                                                                                                                      SNQFTSVLTGKGLSYGGSLIRPBATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
                                                                                                                                                                                     405 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
                                                                                                                                                                                                   GKGGSDFDPKGKSDAEVMRFCQSFMTELORHISYVQDVPAGDIGVGAREIGYLFGQYKRI
                                              TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                                                                                                                                        DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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    The
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                                                                                                                                                                                                                                                                                 69
ABO84396 represent P. aeruginosa polypeptides of the invention. Note: sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                 VROLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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meningococcal protein trafficking; localisation; infection; vaccine;
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                                                                                                                                                    Length 450;
                                                                                                                                                                                               Indels
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                                                                                                                                                  52.1%; Score 1309; DB 7;
59.2%; Pred. No. 7.9e-116;
ive 55; Mismatches 120;
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WPI; 2004-420615/39
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New compositions having outer-membrane vesicles and proteins from Neisseria meningitidis, useful in the field of meningococcal biochemistry, in particular for preventing and/or treating meningococcal infections.

Claim 9; SEQ ID NO 163; 79pp; English

The invention relates to a novel composition comprising outer-membrane vesicles (OWV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OWVs prepared from a second strain of N. meningitidis, but which are not present in OWVs prepared from the first strain. The composition of the invention demonstrates antibacterial and antiniflammatory activities and may be useful in the field of meningococcal biochemistry, in particular the trafficking and localisation of meningococcal infections, as well as in the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MCSB outer-membrane vesicle (OWV)-related membrane protein the invention #XfffffX%X000000000000X8

Sequence 444 AA;

Gaps Query Match S1.8%; Score 1300.5; DB 8; Length 444; Best Local Similarity 57.4%; Pred. No. Se-115; Matches 257; Conservative 72; Mismatches 104; Indels 15; 15;

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46 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV 103 62 g ઠ ઠે

SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG 163 104

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GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR 223 164

343 VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 402 302 YFEKQKPWGV--AAEIALPCATQNELDEEAAKTILANGCYVVAEGANMPSTLGAVEQFIK 359

462 ----NVDLAAGANIAGFTKVADAVKAQG 485

416

Search completed: September 8, 2005, 02:34:15 Job time : 97.0793 secs

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RESULT 1
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2638
1 MQTALVAKPIVACAWVRSAK......GANIAGFTKVADAVKAQGAV 512
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'(cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
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'(cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1774312 seqs, 393823214 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli	Segmence 4, Appli	Sequence 2, Appli	Sequence 2. Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 26, Appl	Sequence 26, Appl	Sequence 66687. A	Sequence 43, Appl	Sequence 65129, A
SUMMARIES	9 US-09-070-844-4	US-10-627-886-4	US-09-070-844-2	US-10-627-886-2	US-09-070-844-24	US-10-627-886-24	US-09-070-844-26	US-10-627-886-26	US-10-282-122A-66687	US-10-988-943-43	US-10-282-122A-65129
90	6	16	- О	16	9	16	0	16	15	18	15
å Query Match Length DB ID	512	512	526	526	487	487	476	476	445	444	444
& Query Match	100.0	100.0	99.4	99.4	95.1	95.1	93.4	93.4	49.6	49.3	49.5
Score	2638	2638	2621	2621	2508	2508	2465	2465	1309	1300.5	1297.5
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41,	App	38,	47,	۷.	45200,	10	338, App	90, Appl	196,	72329,	70,	124,	2, Ap	Ap	17284, A	51278, A	App,	42,	Ap	84,	17,	72961, A	5, Ap	21,	60243, A	App	AD.	82, Appl	98,	93,	10,	App.	
66041		67538																						10621	602	80	6982	82,			6081		
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 6982,	Sequence	Sequence	Sequence	Sequence	Sequence	
-122A-66041	-152	-67538	13947	9839	-45200	-57310	338	06	-58096	-72329	-66870	-74024	2632	340	17284	-51278	617	-48442	859	-43284	-52117	72961	8215	10621	-60243	80	982	82	-53998	-75593	-60810	295	
10-282-122A	10-275-026A	US-10-282-122A-67538	10-369-493-	10-369-493-	10-282-122A	US-10-282-122A-57310	US-10-953-901-338	10-260-877-	10-282-122A	US-10-282-122A-72329	10-282-122A	10-282-122A	US-10-472-928-263	US-10-953-901-340	US-10-369-493-1728	US-10-282-122A-512	10-369-493-617	US-10-282-122A-484	US-10-369-493-859	10-282-122A	US-10-282-122A-5211	US-10-425-114-72961	US-10-369-493-8215	10-369-493-	US-10-282-122A-602	US-11-073-550-80	-09-738-626-6982	US-11-073-550-82	US-10-282-122A-53998	US-10-282-122A-7559	10-282-122A-6081	10-369-493-295	
US-1	us-	us-	-Sn	ns-	ns-	ns-	us-	us-	ns-	ns-	ns-	us-	ns-	us-	-Sn	us-	US-1(-Sn	ns-	us-	-SD	us-	us-	us-	-Sn	ns-	us-0	ns-	-SD	-Sn	US-1(US-10.	
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49.1	49.1	48.8	48.6	47.7	47.7	47.0	47.0	46.9	46.9	46.6	46.6	46.0	45.9	45.9	45.9	45.8	45.7	45.7	45.5	45.5	45.5	45.4	45.3	45.3	45.1	45.1	44.9	44.9	44.8	44.8	44.7	44.7	
1294.5	1294.5	1287.5	1281	1259	1257.5	1239.5	1239.5	1238	1238	1230.5	1230	1214	1212	1211.5	1210.5	1207.5	1205.5	1205.5	1201	1201	1199	1196.5	1195.5	1194	1191	1191	1185	1184	1182.5	1181	1180.5	1180	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	

ALIGNMENTS

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APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik & Saliwanchik
ADDRESSES: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/070,844
                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galnesville STATE: Plorida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
                  Sequence 4, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         32606
US-09-070-844-4
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ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 2638; DB 16, Best Local Similarity 100.0%; Pred. No. 2.7e-228, Matches 512; Conservative 0; Mismatches 0;
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                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/627,886
FILING DATE: 24-U1-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-077-96
APPLICATION NUMBER: 08/725,596
FILING DATE: 06-OCT-96
APPLICATION NUMBER: 08/71,033
      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
05-10-627-886-4
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 512 amino acids TYPE: amino acid
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US-09-070-844-2
; Sequence 2, Application US/09070844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSPWTELQRHISYVQDVPAGDIGVGAREIG 240
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Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND FOLYNUCLECTIDES

THE OF INVENTION: THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KSDTAVYVGDRRKPWELDCQVDIAFPCATONEIDEHDAELLIKHGCQYVVECANMPSTNE
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CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
STREET: 2421 N.W. 41st Street, Suite A-1
STREET: 12421 N.W. 2000 STREET: 2421 N.W. 2000 STREET: 2421 N.W. 2000 STREET: 2421 N.W. 2000 STREET: 2421 N.W. 2000 STREET: 2420 STREET: 242
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2638; DB 9;
100.0%; Pred. No. 2.7e-228;
tive 0; Mismatches 0;
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Publication No. US20040128710A1
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-9100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 512, Conservative
                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                        US-09-070-844-4
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421 QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LÓKAVKOMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, PALLID
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
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                                                                                                             512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPANY ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STRATE: Plorida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: CURROWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                       481 KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                                                           KLERIMKDI YDSAMGPSRRYNVDLAAGANI AGFTKVADAVKAQGAV
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Pred. No. 9.4e-227;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                              Sequence 2, Application US/10627886 Publication No. US20040128710A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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LENGTH: 526 amino a
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity
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US-10-627-886-2
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                                      APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: BEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%; Score 2621; DB 9; Length 526; 97.3%; Pred. No. 9.4e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION NUMBER: 08/725,596
FILING DATE:
FILING DATE:
FILING DATE:
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0; Mismatches 0
                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPAN: (904) 375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 526 amino acids
amino acid
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Matches 512; Conservative
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US20020062495A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Schmidt, Philip
TITLE OF INVENTION: NOVEL POLYBEFTIDES AND POLYNUCLECTIDES
DEHYDROGENASES AND HETHODS OF USE
                                                                                                                              AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
                                                                                                                                                                                                                                                                                             122 YSSAIGPYKGGLRFHPSVNLSIMKFLAPEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                                                                                                                                                                                                                                                                                    182 MRFCQSFWTELORHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGGEYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 SQGYVYEPNGFTREQLQAVQDMKKKNNSARISBYKSDTAVYVGDRRKPWELDCQVDIAFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 GLEMTONEMSLAMTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                                                                                                                                                                                                     YSSAIGPYKGGLRPHPSVNLSIMKFLAPEQIPKNSLTTLPMGGGKGGSDPDPKGKSDAEV
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                                                                                                 27 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTBIFMKDPEQ
                                                                                                                                                                                                                                                                                                                                                           MRFCQSFWTELQRH1SYVQDVPAGD1GVGARE1GYLFGQYKR1TKNYTGVLTPKGQEYGG
                 Length 487;
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STATE: PLOTICE
STATE: PLOTICE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOTICE
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION: WWHER: 09/070,844
FILING DATE: 01-MS-98
FILING DATE: 01-MS-96
FILING DATE: 03-OCT-96
                                                         Indels
               Score 2508; DB 9; L
Pred. No. 1.3e-216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                           ö
95.1%; scc. 100.0%; Pred. No. ... 0; Mismatches
             Query Match
Best Local Similarity 100.
Matches 486; Conservative
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                                                                                                                                                             VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09070844

Sequence 24, Application US/09070844

Sequence 24, Application US/09070844

Setent No. US20020065495A1

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

TITLE OF INVENTION: NELATING THE '- AND -SUBUNITS OF GLUTAMATE

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik Gainewhile

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainewhile

STATE: Florida

CONNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Florpy disk
                                                                                                 241 VPAGDIGVGARRIGYLFGQYKRITKNYTGVLTPKGQEYGGSBIRPEATGYGAVLFVENVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                421 QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                           SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
                                                                                                                                                                                                                                                                                                                                   DMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAPPCATQNBIDBHDAELLIKHGC
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APPLICATION NUMBER: US/09/070,844 FILING APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844 FILING APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844 FILING APPLICATION NUMBER: US/09/070,844 FILING APPLICATION NUMBER: US/09/0725,596 APPLICATION NUMBER: UPI55 REFERENCE/DOCKET NUMBER: UPI55 REFERENCE/DOCKET NUMBER: UPI55 TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-800
INPORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
LENGTH: ABT amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE: NORVATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFISS
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 476 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-070-844-26
     Gainesville
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Best Local Similarity
                     STATE: F
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLITLPMGGGKGGSDFDPKGKSDAEV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
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                                                                                                                                                                                                                                                                                                                                                                                 27 AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
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Patent No. US20020062495A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 Length 487;
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                                                                                                                                                                                                                                                                                                            95.1%; Score 2508; DB 16;
100.0%; Pred. No. 1.3e-216;
ive 0; Mismatches 0;
                                             NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOWMUNICATION INPORMATION:
TELEPAN: (352) 375-8100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
                  FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 486; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAQGAV 512
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                                                                                                                                                                                                                                                                          US-10-627-886-24
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360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
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                                                                                                                                                      9
                                                                                                                              1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFWKDPEQQEFWQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSOGVVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTREQLQAVQDMKKKONSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DABLLI KHGCQYVVEGANMPSTNEA I HKYNKAGI I YCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                       LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512
                                                                                                     37 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                      ..
                                                   0; Indels
93.4%; Score 2465; DB 9;
100.0%; Pred. No. 9e-213;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-627-886-26
; Sequence 26, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
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APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Tamammoro, Kobert
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
TITLE OF INVENTION INDERS: US/10/282,122A
CURRENT APPLICATION NUMBER: 00/206,848
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/203
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKGGSDFDPKGKSDAEVMRFCQSFWTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 249
                                         DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VDAFLERLKRRDFDQPEFHQAVESVLRSLWPFLEANPHYLEAGIIERIVBPERAILFRVP
              DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                          LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 512
                                                                                                                                     LINWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                      Sequence 66687, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oilsen, Kari
APPLICANT: Oilsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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Best Local Similarity 59.2%
Matches 263; Conservative
                                                                                                                                                                                                                                                  US-10-282-122A-66687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE ,- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AVSLQPVFEKRPELLDIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFWKDPEQQEFWQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSRIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LÓRHISYVÓDVPAGDIGVGAREIGYLFGÓYKRITKNYTGVLTPKGÓGYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                      STATE: Floring
COMPUTEY: USA
ZIP: 32606-6669
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRINT APPLICATION DATE: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION NUMBER: US/00/844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/25,596
FILING DATE: 00-OCT-95
APPLICATION NUMBER: 08/25,596
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NUMBE: Lioyd, Jeff
REGISTRANCE/DOCKET NUMBER: UF-155CD3
FILERPHORE: (352) 375-580
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREBET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-627-886-26
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT PELICATION NUMBER: US/10/282,122A
CURRENT PELICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/263,635
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/263,338
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-17
PRIOR PLING DATE: 2001-02-17
PRIOR P
     360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
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57.4%; Pred. No. 1.1e-107;
tive 70; Mismatches 106;
                                                                              Sequence 65129, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Matches 257; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
                                                      487
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APPLICANT:
APPLICANT:
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Publication No. US20050176085A1
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
TITLE OF INVENTION: COMPLEX MIXTURES.
FILE REPERENCE: Proteomics CU2003-269
CURRENT APPLICATION NUMBER: US/10/988,943
CURRENT FILING DATE: 2004-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 AARKVWEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKONVRR-GRIREMAEQFSLQFL 303
                                                                                                                                                                                                                                                        DRRKPWELDCOVDIAFPCATONEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAG 429
                                                                                                                                                                                                                                                                                                                                                               430 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV 488
                                                                                                                                                                                                                                                                                                                                                                                          71 DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV 128
                                                                                                                                                 310 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 369
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GKGGSDPDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL 184
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                                                                              250 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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Best Local Similarity 57.4%; Pred. No. 5.8e-108;
Matches 257; Conservative 72; Mismatches 104;
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249 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 308
                              183 IRNEFISVLIGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ 242
                                                                                               309 YCABLLLEKGAIVLSLSDSQGYVYEPN-GFTREQLQAVQDMKKKNNNSARISEYKSDTAVY 367
                                                                                                                        243 YAAEKAIQLGAKVLIVSDSDGFVLFPDIGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
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                                                                                                                                                                                                                                                                                                                    360 AGILYAPGKASNAGGVATSGLEMSQNAIRLSWARREVDSRLFGIMOSIHESCL----KYG 415
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PLICATION NUMBER: 60/191,078
PRIOR PLICATION NUMBER: 60/206,848
PRIOR PLICATION NUMBER: 60/206,848
PRIOR PLICATION NUMBER: 60/206,948
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,335
PRIOR PLICATION NUMBER: 60/230,335
PRIOR PLICATION NUMBER: 60/230,335
PRIOR PLICATION NUMBER: 60/230,347
PRIOR PLICATION NUMBER: 60/245,578
PRIOR PLICATION NUMBER: 60/245,578
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/257,931
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APPLICANT: Zamudio, Carlos
APPLICANT: Aanudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zaystind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Korsyth, R.
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SEQ ID NO 66041
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49.1%; Score 1294.5; DB 15; Length 444; 57.1%; Pred. No. 2e-107;

Query Match Best Local Similarity

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                                         DVRQLLTRIFMKDPEQQBFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
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  15;
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TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
FILE REFERENCE: GJS-6436
CURRENT APPLICATION NUMBER: US/10/275,026A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/GB01/02003
PRIOR PLIING DATE: 2001-05-08
PRIOR FILING DATE: 2000-05-08
72; Mismatches 105; Indels
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US-10-275-026A-152
Sequence 152, Application US/10275026A
; Publication No. US20040087770A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 152
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Best Local Similarity 57.1*
Matches 256; Conservative
  Conservative
256;
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13947
                                                   72 VRQLLTEIFMKDPEQOEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 129
                                                                                                                                                                     68 WYDDQGKVQVRGYRIQMSSAIGPYKGGLRFHPSVNLSVLKFLAFEQVFKNSLTSLPMGG 127
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       Mismatches 124; Indels
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Best Local Similarity 58.1%; Pred. No. 3.3e-106;
Matches 258; Conservative 59; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: |||||||| |||||: ||| | |
INYVKGANIAGFVKVADAMLAQGVV 449
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas fluorescens
       55;
    259; Conservative
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PALLICATION NUMBER: 06/191,078
PRIOR PALLOR PAILS 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PAPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-105
                                                                                                                                                                                                                                                                                                            243 YAAEKAIQLGAKVLITVSDSNGFVLPPDSGMSEAQLAALIELKEVRRE-RVATYAKEGGLQ 301
                                                                                                                                                                                           427
                                                                                                                                                                                                            302 YFENQKPWGV--AABIALPCATQNELDEBAARTLLANGCYVVAEGANMPSTLGAVEQFIK 359
  ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ 308
                                                                                             YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 367
                                                                                                                                                                                                                                                                               AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY- 486
                        368 VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANNPSTNEAIHKYNK
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                                                                                                                                                                                                                                                                                                                                                                             487 ----NVDLAAGANIAGFTKVADAVKAQG 510
                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SCPTWARE: Patentin version 3.1
SEQ ID NO 67538
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67538, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAZA-67538

Publication No. US2004002912:
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu:
APPLICANT: Zamudio, Carlos
APPLICANT: Manone, Cheryl
APPLICANT: Haselbeck, Robert
VPLICANT: Ohlsen, Kari
PPLICANT: Ohlsen, Kari
"PLICANT: Yakind, Judith
"JICANT: Trawick, John
"CANT: Trawick, John
"CANT: Trawick, John
"CANT: Trawick, John
"ANT: Yamamoto, Robert
"NT: Forsyth, R.
"T: Xu, H.
"INVENTION"
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Best Local Similarity
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Search completed: September 8, 2005, 02:38:54 Job time : 97.8047 secs

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1 MQTALVAKPIVACAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTALOKAVKOMATKAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 2638; DB 2; Length 512; Best Local Similarity 100.0%; Pred. No. 5.7e-235; Matches 512; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                   US-08-541-033A-4
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3884, Ap
4489, Ap
3, Appli
11, Appl
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6657, Ap
6, Appli
5, Appli
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1, Appli
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Sequence 2162, Ap
Sequence 11352, A
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                                                            77; Search time 27.4224 Seconds (without alignments) 1393.764 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Appl:
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     US-10-627-886-4
2638
1 MQTALVAKPIVACAWVRSAK......GANIAGFTKVADAVKAQGAV 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence 1
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Sequence 5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-824-451-24
US-08-541-033A-24
US-08-541-033A-24
US-08-928-921A-20646
US-09-134-000C-3884
US-09-134-000C-3889
US-09-134-000C-3884
US-09-583-110-4489
US-08-886-640-3
US-08-886-640-3
US-08-886-640-3
US-08-489-039A-137
US-09-543-611A-657
US-09-543-611A-6557
US-09-543-611A-6557
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5-09-543-681A-6657
5-08-508-761B-6
5-09-171-337A-5
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US-09-902-540-11352
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                               513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                            September 8, 2005, 02:01:27
                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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46.3
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1143
1037.5
1012
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                                                            Run on:
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Sequence 22, Appl
Sequence 20, Appl
Sequence 1153, Ap
Sequence 23, Appl
Sequence 7622, App
Sequence 7622, App
Sequence 7622, Appl
Sequence 7623, Appl
                                12638, A
2, Appli
6130, Ap
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2, Appli
2, Appli
122, App
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Patent No. 5879941
GENERL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Phillip
TITLE OF INVENTION: DEHYDROGENASES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                   Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
Sequence
US-09-239-303-9
US-09-902-540-12638
US-09-902-540-12638
US-09-328-352-6130
US-09-489-039A-13935
US-08-461-990B-22
US-08-461-990B-22
US-09-538-092-1153
US-09-538-092-1153
US-09-949-016-7622
US-09-949-016-7622
US-09-949-016-7623
US-09-940-019-7923
US-09-940-019-7923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 512 amino acids
amino acid
     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2421 N.W. 4
CITY: Gainesville
STATE: Florida
COUNTRY: USA
  219

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us-10-627-886-4.rai

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RESULT 3
US-08-541-033A-2
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                                                                                                                                                                                                                                                                                                                                                    241 YLFGQYKRITKNYTGVLTPKGQBYGGSBIRPBATGYGAVLFVBNVLKDKGBSLKGKRCLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM 480
EGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08028451

Patent No. 5985634

GENERAL INFORMATION:
APPLICANT: Miller, Philip
ITILE OF INVENTION: NOVEL POLYERTIDES AND POLYNUCLEOTIDES
ITILE OF INVENTION: BELATING TO THE - AND -SUBUNITS OF GLUTAMATE
ITILE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
ITILE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREE: 2421 N.W. 41st Street, Suite A-1
CTTY: Gaineaville
STATE: Florida
COMPUTE: READABLE FORM:
MEDIUM TYPE: BIP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION D
                            ERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKN
                                                                                                                                      SLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSPMTBLQRHISYVQDVPAGDIGVGAREIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKKNNSARISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 KSDTAVYVGDRRKPWELDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNE
                                                                                                                                                                                                                                                                                                                          YLPGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLV
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WhileLock, Ted W.
REGISTRATION NUMBER: UF155
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 4:
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LENGTH: 512 amino acids
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US-08-828-451-4
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| Sequence 2, Application US/08541033A
| Patent No. 5879941
| GENERAL INFORMATION:
| APPLICANT: Schmidt, Robert R.
| APPLICANT: Miller, Philip
| TILLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
| TILLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| TILLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| TILLE OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Saliwanchik & Saliwanchik
| STREET: 2421 N.W. 41st Street, Suite A-1
| CITY: Gainesville
| STRATE: Florida
| CONNTRY: USA
                                                                                                                                                                                                                                                          1 MQTALVAKPIVACAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTALQKAVKQMATKAGT
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPICATION: 435
                                                                                                                     ; Score 2638; DB 2;
; Pred. No. 5.7e-235;
0; Mismatches 0;
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                                                                                                                          100.0%;
                                                                                                                                                  Best Local Similarity 100.
Matches 512; Conservative
                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-828-451-4
amino acid
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61 LQKAVKQMATKAGTEGLVHGIRNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 120
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                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2621; DB 2;
Pred. No. 2.2e-233;
0; Mismatches 0;
                                                                                                                                                 CLASSIPRICATION:
CLASSIPRICATION:
PRIOR APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 24, Application US/08541033A
; Patent No. 5879941
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                                                                                                                                                                                                                                                                                                                                                                                                    : 526 amino acids
amino acid
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Best Local Similarity 97.3
Matches 512, Conservative
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| Patent No. 5985634
| CENERAL INFORMATION:
| APPLICANT: NTORMATION:
| APPLICANT: Miller, Philip
| TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
| TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
| CORRESPONDENCES: Allwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
| CITY: Gainesville | CITY: Gainesville |
| STREET: Lorida | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
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                                                                                                                                                                                                                                                                          Length 526;
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                                                                                                                                                                                                                                                                       Score 2621; DB 2;
Pred. No. 2.2e-233;
0; Mismatches 0;
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION: (904) 375-800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
                                                                                                                                                                                                                                                                   Query Match 99.4%;
Best Local Similarity 97.3%;
Matches 512; Conservative
                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                amino acid
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                  US-08-541-033A-2
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87 QEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ 146
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                                                                                                                                                                                                                                                                        Sequence 24, Application US/08828451
| Patent No. 598534
| GENERAL INFORMATION:
| APPLICANT: Schmidt, Robert R.
| APPLICANT: Miller, Philip
| TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Sulte A-1 CITY: Gainesville STATE: Plorida CUNTRY: USA COUNTRY: USA COUNTRY: MADABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REPERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INPORMATION:
TELERAN: (904) 375-8100
INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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Matches 486; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: SALIWANCE
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                                                                                                            482 KAQGAV 487
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US-08-828-451-24
                                                                                                                                                                                                                                                US-08-828-451-24
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GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Milet, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
CONNTRY: USA
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/CATION INPORMATION:
TELECOMMUNICATION INPOR
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Best Local Similarity 100.0
Matches 486; Conservative
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MOLECULE TYPE: protein
US-08-541-033A-24
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241 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG 300
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                               121 GLRFHPSVNLSIMKFLAFEQIFKONSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFWTE 180
                                                                                                                                                                                                                                                                                                                                                                           361 DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 420
    157 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFWTE 216
                                                                                                                                                                                                                                                                                                                                                  DAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS 456
                                                                                                                       181 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                         GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                            337 FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATONEIDEH
                                                                                       LORHISYVODVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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APPLICANT: Schmidt, Robert R.
APPLICANT: Milet, Philip
TITLE OF INVENTION: NOVEL POLYBEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.4%; Score 2465; DB 2; I
100.0%; Pred. No. 4.9e-219;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/08828451
Patent No. 5985634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: UP15
RELECOMMUNICATION INFORMATION:
TELEFONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36,965
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 476 amino acida TYPE: amino acid
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Best Local Similarity 100.
Matches 476; Conservative
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MOLECULE TYPE: protein
US-08-828-451-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-828-451-26
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                                                                 SQGYVYEPNGFTREQLQAVQDMKKKONSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 361
                                                                                                                            CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS 446
                                                                                                                                                    CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS 421
                                                                                                                                                                                                                                        SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD 301
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                                          SQGYVYBPNGFTREQLQAVQDMKKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: School Robert R.
APPLICANT: School Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSER: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 STREET: 2421 N.W. 41st Street, Suite A-1 STATE: Plorida COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IB PC COMPUTER: PS PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/541,033A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-8800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
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Best Local Similarity 100.
Matches 476; Conservative
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 467
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SNQFTSVLTGKGLSYGGSLIRPEATGPGCVYPAQEMLKDRGRGFDGQRVAISGSGNVAQY
                                                                          IIYCPGKAANAGGVAVSGLEMTONRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
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                                                    CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
                                                                                                                          DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
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                                                                                                                                                                                                                                                                      DLAAGANIAGFTKVADAVKAQGAV
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US-09-328-352-5725
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Matches 256; Conservative
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US-09-328-352-5725
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Sequence 20646, Application US/09252991A

Sequence 20646, Application US/09252991A

Sequence 20646, Application US/09252991A

Sequence 20646, Application US/09252991A

Patent No. 6551795

REBERTAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20646
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                                                                                                          AVSLQPVFEKRPELLPIPKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
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                MDATTGDPTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                     AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                          GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
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49.6%; Score 1309; DB 4; Length 450;
Best Local Similarity 59.2%; Pred. No. 3e-112;
Matches 263; Conservative 55; Mismatches 120; Indels
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ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-20646
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72 VRQLLTBIFMKDPBQQBFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 129
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8 IQSVFETVKARNGHEAEFLQAVEEFFNTLEPVFEKHPEYIEENILARITEPERVVSFRVP
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.3%; Score 1221; DB 4; Length 4
55.7%; Pred. No. 4.1e-104;
Live 64; Mismatches 125; Indels
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APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, Maria V
TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GE
TITLE OF INVENTION: METHODS OF USE THEREOF
ITLE OF SEQUENCES: 7
CORRESPONDES: ADDRESS: ADDRESSE: 
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
SEQ ID NOS: 5322
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 KDYLAGANIAAFENVANAMIAQGIV 448
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,640
                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae
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US-08-886-640-3
; Sequence 3, Application US/08886640
; Patent No. 5998700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 55.73
Matches 248; Conservative
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Patent No. 6699703
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPRENUE:
FILE REPR
                                                                                                                                                          Sequence 3884, Application US/09134000C

Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BUTERCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 AMEKATELGATVITCSDSSGFVYDPEGI---DVALVKELKEKNRE-RISKYVETRKGATY 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 250; Conservative
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Best Local Similarity
                                                                                                                          -09-134-000C-3884
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LENGTH: 448
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STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,235
FILING DATE: 27-UN-1997
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                                                                                                                                                                                                                                         LENGTH: 447 residues
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                    CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. 6328573
GENERAL INFORMATION:
APPLICANT: Lightfoot, David A.
APPLICANT: Lightfoot, Maria E. Vidal
TITLE OF INVENTION: METHODS OF USE THEREOF
ITILE OF INVENTION: METHODS OF USE THEREOF
OORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                          Query Match 45.5%; Score 1201; DB 2; Best Local Similarity 54.0%; Pred. No. 2.9e-102; Matches 241; Conservative 67; Mismatches 128;
        FILING ARE: 01-01-1997
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,058
FILING DATE: 02-010-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL K.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 81163/241766
TELEPHONE: (202)-861-3503
TELEPHONE: (202)-861-3503
TELEPAX: (202)-861-3503
TELEPAX: (202)-861-3503
TELEPAX: (202)-861-3503
TELEPAX: (202)-861-363
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYRANDENDESS: not relevant
TOPOLOGY: not relevant
TOPOLOGY: not relevant
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01-JUL-1997
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72 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 369
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                                                                        Gaps
                                                                 10;
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| Patent No. 5573945 |
| GENERAL INPORMATION: |
| APPLICANT: ONO, EIJI |
| APPLICANT: TSUJIMOTO, NOBUHARU |
| APPLICANT: TSUJIMOTO, NOBUHARU |
| APPLICANT: MATSUI, KAZUHIKO |
| TITLE OF INVENTION: L-GLUTAMIC ACID BY PERMENTATION |
| TITLE OF INVENTION: L-GLUTAMIC ACID BY PERMENTATION |
| CORRESPONDENCES: 11 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
Length 447;
                                                                 Indels
Query Match 45.5%; Score 1201; DB 3;
Best Local Similarity 54.0%; Pred. No. 2.9e-102;
Matches 241; Conservative 67; Mismatches 128;
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72 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 129
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STRATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/370,193A
FILING DATE: 09-JAN-1995
CLASSIFTCATION: 435
ATTOCNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F: 24,618
REGISTRATION WUMBER: 24,618
REGISTRATION WUMBER: 24,618
REGISTRATION WUMBER: 10-714-0
TELEFAX: 703-413-3000
TELEFAX: 703-413-220
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TELEFAX: 703-413-220
TELEFAX: 703-413-3000
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Best Local Similarity 54.0%; Pred. No. 3.6e-102; 
Matches 241; Conservative 67; Mismatches 128;
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Search completed: September 8, 2005, 02:12:06 Job time : 30.4224 secs

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DT 01-MA
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DB Gluta
GN Name
OS Plasm
OC Eukar
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Best Local S
SEQUENCE FROM N.A.

STRAIN=FCQ 27;

YUAN P., Stewart T.S.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
EMBL; AF098675; AAD11789.1; -.

HSSP; P24295; 1AUP.

GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0016520; P:amino acid metabolism; IEA.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006095; GLFV_dehydrog_N.

Pfam; PF02812; GLFV dehydrog_N; 1.

Pfam; PF02812; GLFV dehydrog N; 1.

PRINTS; PR000082; GLFDHDRGNASE.
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InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_Y.
Pfam; PF02812; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_DEHYDROGENASE; 1
NON TER
SEQUENCE 437 AA; 47861 MM; 752055541
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9TXS8; PRELIMINARY;
Q9TXSB;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-UN-2003 (TrEMBLrel. 2
01-UN-2003 (TrEMBLrel. 2
Glutamate dehydrogenase.
Name=GDH;
                                                                                                                                                                                                                                                                                                                                              rrasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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0 (TrEMBLrel. 13,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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Pred. No. 9.9
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Best Local Similarity
Matches 258; Conserv
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SEQUENCE
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442 AA; 49432 MW; 9D3F8AA679CCE4CC
                                                                                                                           LNVKVLTLSDSNGYVYEPNGFTHENLEFLIDLKEE-KKGRIKEYLNHSSTAKYF-PNEKP
                                        SKAANAGGVAISGLEMSONFOFSHWTRETVDEKLKEIMRNIFIACSENALKYTKNKYDLO
                                                   GKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLA
                                                                                 WELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCP
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AGANIAGFLKVAESYIEQG
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                                                                                                                                     KGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVGDRRKP
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Search completed: September 8, 2005, 02:43:28 Job time : 95.6807 secs

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O9Z3C4;

O1-MAY-1999 (TrEMBLrel. 10, Creff o1-MAY-1999 (TrEMBLrel. 20, Last o5-JUL-2004 (TrEMBLrel. 27, Last opening of the control o
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Best Local S
Matches 266
Ansari F.;
Thesis (1994), University of EMBL; Y18494; CAA77192.1; -
EMBL; Y15166; CAA75437.1; -
HSSP; P24295; IAUP.
GO; GO:0004354; F:glutamate
                                                                                                                                                                                                                                                                                                             Thesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gam
Pseudomonadaceae; Pseudomonas
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STRAIN=PAC1;
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    F:glutamate dehydrogenase (NADP+) activity;
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10, Last sequence update)
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Pred. No. 8e-79;
4; Mismatches 1
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Best Local Sim
Matches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7YZU7
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfinits; PR000082; GLFDHDRGNASE.
                                             PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
"Evolution of glutamate dehydrogenase genes: evidence for transfer within and between prokaryotes and eukaryotes.";
BMC Evol. Biol. 3:14-14(2003).
EMBL; AF533886; AAP83853.1; -.
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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SEQUENCE 445 AA; 48532 MW; B00DDE
                                                                                                                                                                                                                                                                                Trichomonas vaginalis.
Eukaryota; Parabasalidea; Trichom
Trichomonadidae; Trichomonadinae;
                                                                                                                                                                                                                                                                                                                                                                            Glutamate dehydrogenase
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=5722;
                                                                                                                                                                                                                                                                                                                                                 Name=gdh;
    GO:0016491; F:oxidoreductase activity; IF GO:0006520; P:amino acid metabolism; IEA.
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25, Last so
26, Last as
(Fragment)
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; Pred. No. 9.4e-79;
56; Mismatches 118;
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Last annotation update)
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                                                                                                                        Query Match
Best Local S
Matches 266
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01-MAY-1999
01-MAY-1999
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InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog, 1.
PFINTS; PR00082; GLFU_DEHYDROGENASE;
PROSITS; PS00074; GLFV_DEHYDROGENASE;
Oxidoreduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li L.H., Li M., Wu Y.S., Wang Submitted (JUN-2001) to the EW EMBL; Y12927, CAR73390.1; --
EMBL; AY040586; AAK77969.1; --
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01-MAY-1999 (TYENBLYE]. 10, Last sequence update)
05-JUL-2004 (TYENBLYE]. 27, Last annotation update
Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
                                                                                                                                                                                                                                     Oxidoreductase.
SEQUENCE 470
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Krauth-Siegel R.L.;
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MEDLINE=99089647; PubMed=9874251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Glutamate dehydrogenase, the marker protein of Plasmodium falciparum. Cloning, expression and characterization of the malarial enzyme.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P; P24295; IAUP.
GO:0004354; F:glutamate dehydrogenase (NADP+)
GO:0016491; F:oxidoreductase activity; IEA.
GO:0006520; P:amino acid metabolism; IEA.
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                                                                                                                                                     Similarity
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llarity 55.2%;
Conservative 6
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he BMBL/GenBank/DDBJ
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                                                                                                                        Score 1286.5; D
Pred. No. 8e-79;
4; Mismatches 1
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRO
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;

Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

Gardner M.J., Hall N., Pelson K.E., Bowman S., Paulsen I.T., James K.,

Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S.,

Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

Fraser C.M., Barrell B.;

"Genome sequence of the human malaria parasite Plasmodium
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Q8ILTO;
01-MAR-2003
01-MAR-2003
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Bukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADP-specific glutamate ORFNames=PF14_0164;
                                                                                                                                                                                                                                                                                   EMBL; AE014818; AAN
HSSP; P24295; IAUP.
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                                                                                                                                                                                                                                                                                                                                             Nature 419:498-511(2002).
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Best Local S
Matches 256
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GO; GO:0004354; F:glutamate dehydrogenase (NADP+) act
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFV_dehydrog_N; 1.
PRINTS; PS00074; GLFV_DEHYDROGENASE; 1.
Complete proteome; Oxidoreductase.
SEQUENCE 444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64
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01-OCT-2000 (TrEMBLrel. 25, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Glutamate dehydrogenase (EC 1.4.1.4).
Name=gdhA; OrderedLocusNames=NMA1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Z2491 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919, DOJ=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Klee S.R., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jayels K., Davis P., Devlin K., Feltwell T., Quail M.A.,
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL162757; CABBO
PIR; B81825; B81825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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EMBL; AL162757; CAB85184.1; -.
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                                                                                                                                             GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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IRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ
                                 ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
                                                                                                                                                                                                                               TWODDKGQVQVNRGYRVQMSSAIGPYKGGLRFHPTVDLGVLKFLAFEQVFKNALTTLPMG
                                                                                                                                                                                                                                                                                                                                              DLNTLFANLKQRNPNQEPFHQAVEEVFMSLDPFLAKNPKYTQQSLLERIVEPERVVMFRV
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                                                                                                               GGKGGSDFDPKGKSDAEVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.18;
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                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 259; Conserv
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088023; TremBLrel. 24,
01-JUN-2003 (TremBLrel. 24,
01-JUN-2003 (TremBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJINE-22433060; PubMed=12534463;
Melson K.E., Weinel C., Paulisen I.T., Dodson R.J., Hilbert H.,
Melson K.E., Weinel C., Paulisen I.E., Gill S.R., Pop M., Holmes M.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamate dehydrogenase.

Name=gdhA; OrderedLocusNames=PP0675;

Pseudomonas putida (strain KT2440).

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00074; GLFV_DEHYDROGENASE; Complete proteome.
SEQUENCE 449 AA; 48871 MW; EF17331
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006095; GLFV_dehydrog.C.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
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HSSP; P24295; 1AUP.
TIGR; PP0675; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0006520; P:amino acid metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
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89
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                                YFENQKPWGV--AAEIALPCATQNELDEEAAKTLLANGCYVVAEGANWPSTLGAVEQFIK
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                                                                                                                                        VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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  WVDDQGKVQVNRGYRIQMSSAIGPYKGGLRFHPSVNLSVLKFLAFEQVFKNSLTSLPMGG
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Last
                                                                                                                                                                                                                        Score 1287.5; DB
Pred. No. 6.4e-79;
5; Mismatches 124
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annotation updat
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NYVKGANIAGFVKVADAMLAQGVV

445

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Query Match
Best Local Similarity
Matches 263; Conserv
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
Pfam; PF00208; GLFV dehydrog; 1.
Pfam; PF00208; GLFV dehydrog; 1.
PRINTS; PR000082; GLFV dehydrog; N; 1.
PRINTS; PR000082; GLFV DEHYDROGENASE; 1.
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STRAIRMATCC 15692 / PAO1;

MEDLINE=20437373; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kasa A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HVJ7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; H83072; H83072.
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
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Name=gdhA; OrderedLocusNames=PA4588;
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                                                                                                                                                        DRRKPWELDCQVDIAFPCATQNEIDEHDABLLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                                                                                                        TKNYTGVLTPKGQEYGGSEIRPBATGYGAVLFVBNVLKDKGESLKGKRCLVSGAGNVAQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
                       DLAAGANIAGFTKVADAVKAQGAV
                                                                               IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
                                                                                                                                      EGRRPWGLAC
                                                                                                                                                                                                                                             CABLLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
                                                                                                                                                                                                                                                                                    SNOFTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
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                                                        ILYAPGKASNAGGVAVSGLEMSQNAMRLRWSEGEVDTKLHGIMQSIHHACLLYGEEQGRV
                                                                                                                                                                                                          AARKVMEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL
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                                                                                                                                  DIALPCATQNELDAEDARRILLANGCVCVAEGANMPSTLEAVDLFLEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1309; DB
Pred. No. 2.2e-
55; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
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Best Local S
Matches 257
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
PRINTS; PR000082; GLFV_dehydrog_N; 1.
PRINTS; PR000082; GLFV_DEHYDROGENASE; 1.
COMPlete proteome.
SEQUENCE 444 AA; 48490 MW; 8B2CFCCA89EF7D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JY71;
Q9JY71;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grandi G.,
Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-MC58 / Serogroup B;

MEDLINE-20175755 pubMed=10710307; DOI=10.1126/science.287.5459.1809;

Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

Relson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

Dougherty B.A., Mason T.M., Ciecko A., Parkesy D.S., Blair E.,

Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,

Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,

Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-UNN-2003 (TrEMBLrel. 24, Last annotation
Glutamate dehydrogenase, NADP-specific.
OrderedLocusNames=NMB1710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P24295;
TIGR; NMB1710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (serogroup B)
Bacteria; Proteobacteria; Betaproteo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae;
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H81050; H81050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                            GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGARBIGYLFGQYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                               SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                                           ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                 TWODDKGQVQVNRGYRVQMSSAIGPYKGGLRFHPTVDLGVLKFLAFEQVFKNALTTLPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLNTLFANLKORNPNOEPFHOAVEEVFMSLDPFLAKNPKYTOOSLLERIVEPERVVMFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRV
                                                      YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ
                                                                                                             YCABILIEKGAIVISISDSQGYVYEP-NGFTREQIQAVQDMKKKNNSARISEYKSDTAVY
                                                                                                                                                                          IRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ
                                                                                                                                                                                                                                                                                             GGKGGSDFDPKGKSDAEVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local S
Matches 261
                                                                                                                                  P28724; Q24961;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 43, Last annotation update)
29-MAR-2004 (Rel. 43, Last annotation update)
NADD-specific glutamate dehydrogenase (EC 1.4.1.4)
dependent glutamate dehydrogenase).
Glardia lambila (Glardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AACB01000014; EAA41919.1; -.
HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase activity;
GO; GO:0006520; P:amino acid metabolism; IE
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
                                                                                                                                                                                                                                                      DHE4
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Pfam; PF00812; GLFV dehydrog N; 1.

PRINTS; PR000082; GLFDHDRGNASE.

PROSITE; PS00074; GLFV DEHYDROGENASE; 1.

SEQUENCE 449 AA; 49734 MW; 2397834FBEBCAEE2 CRC64;
                                  Yee J., Dennis P.P.;
"Isolation and characterization of a N
dehydrogenase gene from the primitive
J. Biol. Chem. 267:7539-7544(1992).
SEQUENCE OF 59-261 FROM N.A. MEDLINE=96155200; PubMed=8587793;
                                                                                         SEQUENCE FROM N.A. MEDLINE=92218410;
                                                                                                                             NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
                                                                                                                                                                                                                                                     GIALA
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                                                                                                                                                                                                                                                                                                                      HPKNYQMGANIAGFLKVADSMIEQGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                             GDRRKPWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELLLEKGAIVLSISDSQGYVYBPNGFTREQLQAVQDMKKKNNSARISEYKS---DTAVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTGVLTGKNVKWGGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKNVLLSGSGNVAQFAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
                                                                                                                                                                                                                                                                                                                                               --VDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                                                                                                                                                                                                                                                                                   AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 487
                                                                                                                                                                                                                                                                                                                                                                                                                             G--KKPWECFEGOVDCIMPCATONEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA
                                                                                                                                                                                                                                                                                                                                                                          KGVMYGPAKASNAGGVSVSGLEMSONSVRLOWTAEEVDQKLRGIMRGIFVACRDTAKKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLIQLGAKVLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                                         PubMed=1559991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1327.5;
Pred. No. 1.2e
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                 NADP-dependent
                                                                                                                                                                                                                                                                                                                                                 512
                                                                                                                                                                                                                                                     449
                                                  NADP-dependent glutamate eucaryote Giardia lamblia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 2;
.2e-81;
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                                                                                                                                            Giardia
                                                                                                                                                                                   (NADP-GDH)
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                                                                                                                                                                                  (NADP-
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Matches 260
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InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLEV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PFNNTS; PR000027; GLFDHDRGNASE; 1.
PROSITE; PS000074; GLFV_DEHYDROGENASE; 1.
PROSITE; PS000074; GLFV_DEHYDROGENASE; 1.
NADP; Oxidoreductase.
ACT_SITE 125 By similari
CONFLICT 249 249 I -> L (in
SEQUENCE 449 AA; 49766 MW; 5497B3520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamate dehydrogenase locus.";
Parasitology 112:1-12(1996).
-!- CATALYTIC CATYLITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarat.
-!- NH(3) + NADPH.
-!- SUBUNIT: Homohexamer (By similarity).
-!- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
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EMBL; U47632; AAB05400.1; -.
PIR; A42489; A42489.
HSSP; P24295; LAUP.
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                                                                                                                                                                                                                                                                                                                                                                                   DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK 191
                                                                                                                                    GDRRKPWE-LDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                               IEELIAVIKQRDGHMTEFRQAVEEVVDSLKVIFEREPKYIFIFERMLEPERVIIFRVPWM
HPKNYOMGANIAGFLKVADSMIEQGCV
                           --VDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                      G--KKPWECFEGOMDCIMPCATONEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA
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I -> L (in Ref. 2).
; 5497B35209B549F6 CRC64;
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1; Mismatches
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RESULT Q9HVJ7

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GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR005135; Exo endo phos.
InterPro; IPR006095; GLFV dehydrog C.
InterPro; IPR006096; GLFV dehydrog C.
InterPro; IPR006097; GLFV dehydrog N.
InterPro; IPR006097; GLFV dehydrog N.
Pfam; PF00372; Exo endo phos; 1.
Pfam; PF00208; GLFV dehydrog N; 1.
PFAm; PF00208; GLFV dehydrog N; 1.
PFAm; PF00208; GLFV dehydrog N; 1.
PFAM; PF00208; GLFV DEHYDROGENASE; 1.
PROSITE; PR00082; GLFV DEHYDROGENASE; 1.
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                                                                                             Q7YZU9;
Q7YZU9;
01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
Glutamate deb
                                                  Spironucleus barkhanus.
Eukaryota; Diplomonadida;
NCHI TaxID=103874;
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-i- CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
SEQUENCE FROM N.A.
STRAIN=ATCC 50380;
PubMed=12820901; DOI=10.118
Andersson J.O., Roger A.J.;
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e dehydrogenase
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            DOI=10.1186/1471-2148-3-14;
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Pred. No. 2
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annotation update)
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RESULT 5
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AC Q7R3
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RC STR2
RA MOLT
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EMC EVOL. Biol. 3:14-14(2003).

REMBL; AF533884; AAP83851.1; -.

REMSP; P24295; 1AUP.

GO; GO:0016491; F:oxidoreductase activity; IEA.

RGO; GO:0016491; F:oxidoreductase activity; IEA.

RGO; GO:0016520; P:amino acid metabolism; IEA.

RGO; GO:0016520; F:amino acid metabolism; IEA.

RINEPTO; IPR006095; GLFV_dehydrog.

RINTEPTO; IPR006095; GLFV_dehydrog.

RINTEPTO; IPR006095; GLFV_dehydrog.

RINTEPTO; IPR006095; GLFV_dehydrog.

RPfam; PF00208; 
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Best Local Similarity
Matches 262; Conserv
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Q7R3N7;
Q7R3N7;
01-MAR-2004 (TEMBLrel. 26, I
01-MAR-2004 (TEMBLrel. 26, I
01-MAR-2004 (TEMBLrel. 26, I
01-MAR-3030 (TEMBLREL. 26, I
GLP 39 39379 38030.
Giardia lamblia ATCC 50803.
Bukaryota; Diplomonadida; Hex
                     Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gill Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/CenBank/DDBJ databases
-1- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                        SEQUENCE FROM
STRAIN=WB C6;
                                                                                                                                                                                                                                                                               NCBI_TaxID=184922;
   EMBL/GenBank/DDBJ whole
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Pred. No. 1.1e-
65; Mismatches
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Last annotation update)
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D QBILF7

C QBILF7;

C QBILF7;

D 1-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Glutamate dehydrogenase, putative.

GN ORFNames=PF14 0286;

OS Plasmodium falciparum (isolate 3D7).

CS Plasmodium falciparum (isolate 3D7).

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plas
        RESULT RESULT OF THE PROPERTY 
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MEDIINE=22255705, PubMed=12368864, DOI=10.1038/nature01097;

MEDIINE=22255705, PubMed=12368864, DOI=10.1038/nature01097;

A Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

A Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

A Carlton J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

A Chan M.S., Nene V., Shallom S.J., Sub B., Peterson J., Angiuoli S.,

A Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

A Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

A Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

A McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,

A Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

A Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

T "Genome sequence of the human malaria parasite Plasmodium

T falciparum.";

PMBIL. ABO14620. ANNIGORO 1.
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Best Local S
Matches 486
EMBL; AB014820; AAN36899.1; -. HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase ac GO; GO:0006520; P:amino acid metabo InterPro; IPR006095; GLFV_dehydrog
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3; Mismatches 1
                                 metabolism; IEA.
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Best Local Similarity
Matches 267; Conserv
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Q7RQ39;
01-MAR-2004
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Eukaryota; Alveolata; Apicomplexa;
MCBI_TaxID=73239;
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STRAIN=17XNL;
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01-MAR-2004 (TrEMBLrel.
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Pfam; PF00208; GLFV_dehydrog; 1.

Pfam; PF02812; GLFV_dehydrog N; 1.

PRINTS; PR000082; GLFDHDRGNASE

PROSITE; PS00074; GLFV DEHYDROGENASE; 1.

SEQUENCE 510 AA; 57343 MW; AC400045297AC64F
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InterPro; IPR006097; GLFV_dehydrog_N.
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                                                                                                                                     ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVG
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                                                           IILCPSKAANAGGVAVSGLEMSQNSMRLQWTHQETDMKLQNIMKSIYEQCHNTSKIYLNE
                                                                                      IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY--N
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Pred. No. 8.
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Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. II, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., valebry S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.
Carucci D.J.; "Genome sequence and comparative analysis parasite Plasmodium yoelii yoelii.";
                                                                                                                                                                                                                                                                                                                                                                       PubMed=12368865; DOI=10.1038/nature01099;
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re greater than or equal to the score of the result being printed,
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1: uniprot_sprot:*
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	1199	1200	1200.5	1201	1202	1205.5	1205.5	1205.5	1206.5	1210.5	1212	1214	1214.5	1225
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1	097129	Q6ajb1	060996	P00370	Q88xm9	Q7weu7	Q64q81	Q9rtn9	Q7vsn6	Q9kb34	Q97qb4	Q8dpg0	P95544	Q9aiw1
	clostridium	desulfotale	trypanosoma	escherichia	lactobacill	bordetella	bacteroides	deinococcus	bordetella	bacillus ha	Btreptococc	streptococc	prevotella	streptococc

ALIGNMENTS

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                           InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
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Pfam; PF02812; GLFV dehydrog; 1.
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By similar:
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DHE4 (CHISO STANDARD; PRT; 523 AA.

P28998;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

29-MAR-2004 (Rel. 43, Last annotation update)

NADP-specific glutamate dehydrogenase (EC 1.4.1.4)
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EMBL; X58831; CAA41635.1; ALT_SEQ.
PIR; S17949; S17949.
HSSP; P24295; IAUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92032762; PubMed=1718478; Cock J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.; "A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella
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Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
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Plant Mol. Biol. 17:1023-1044(1991).
      SEQUENCE
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